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(54) Title: NOVEL NUCLEIC ACID MOLECULES FROM MAIZE AND THEIR USE FOR THE PRODUCTION OF MODIFIED STARCH (57) Abstract Nucleic acid molecules are described encoding a starch granule-bound protein from maize as well as methods and recombinant DNA molecules for the production of transgenic plant cells and plants synthesizing a modified starch. Moreover, the plant cells and plants resulting from those methods as well as the starch obtainable therefrom are described.		

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**Novel nucleic acid molecules from maize and their use for the
production of modified starch**

The present invention relates to nucleic acid molecules encoding a starch granule-bound protein from maize as well as to methods and recombinant DNA molecules for the production of transgenic plant cells and plants synthesizing modified starch. The invention also relates to the transgenic plant cells and plants resulting from these methods and to the starch obtainable from the transgenic plant cells and plants.

The polysaccharide starch, which constitutes one of the most important storage substances in plants, is not only used in the area of foodstuffs but also plays a significant role as a regenerative material in the manufacturing of industrial products. In order to enable the use of this raw material in as many areas as possible, it is necessary to obtain a large variety of substances as well as to adapt these substances to the varying demands of the processing industry.

Although starch consists of a chemically homogeneous basic component, namely glucose, it does not constitute a homogeneous raw material. It is rather a complex mixture of various types of molecules which differ from each other in their degree of polymerization and in the degree of branching of the glucose chains. One differentiates particularly between amylose-starch,

a basically non-branched polymer made up of α -1,4-glycosidically branched glucose molecules, and amylopectin-starch which in turn is a mixture of more or less heavily branched glucose chains. The branching results from the occurrence of α -1,6-glycosidic interlinkings.

The molecular structure of starch which is mainly determined by its degree of branching, the amylose/amylopectin ration, the average chain-length and the occurrence of phosphate groups is significant for important functional properties of starch or, respectively, its watery solutions. Important functional properties are for example solubility of the starch, tendency to retrogradation, capability of film formation, viscosity, pastification properties, i.e. binding and gluing properties, as well as cold resistance. The starch granule size may also be significant for the various uses. The production of starch with a high amylose content is particularly significant. Furthermore, modified starch contained in plant cells may, under certain conditions, favorably alter the behavior of the plant cell. For example, it would be possible to decrease the starch degradation during the storage of the starch-containing organs such as seeds and tubers prior to their further processing by, for example, starch extraction. Moreover, there is some interest in producing modified starches which would render plant cells and plant organs containing this starch more suitable for further processing, such as for the production of popcorn or corn flakes from maize or of French fries, crisps or potato powder from potatoes. There is a particular interest in improving the starches in such a way, that they show a reduced "cold sweetening", i.e. a decreased release of reduced sugars (especially glucose) during long-term storage at low temperatures.

Starch which can be isolated from plants is often adapted to certain industrial purposes by means of chemical modifications which are usually time-consuming and expensive. Therefore it is

desirable to find possibilities to produce plants synthesizing a starch the properties of which already meet the demands of the processing industry.

Conventional methods for producing such plants are classical breeding methods and the production of mutants. Thus, for example, a mutant was produced from maize synthesizing starch with an altered viscosity (US patent specification 5,331,108) and a maize variety (waxy maize) was established by means of breeding the starch of which consists of almost 100% amylopectin (Akasaka and Nelson, J. Biol. Chem. 241 (1966), 2280-2285). Furthermore, mutants of maize and pea have been described which synthesize starches with a high amylose content (70% in maize or up to 50% in pea). These mutants have so far not been characterized on the molecular level and therefore do not allow for the production of corresponding mutants in other starch-storing plants.

Alternatively, plants synthesizing starch with altered properties may be produced by means of recombinant DNA techniques. In various cases, for example, the recombinant modification of potato plants aiming at altering the starch synthesized in these plants has been described (e.g. WO 92/11376; WO 92/14827). However, in order to make use of recombinant DNA techniques, DNA sequences are required the gene products of which influence starch synthesis, starch modification or starch degradation.

Therefore, the problem underlying the present invention is to provide nucleic acid molecules and methods which allow for the alteration of plants in such a way, that they synthesize a starch which differs from starch naturally synthesized in plants with respect to its physical and/or chemical properties and is therefore more suitable for general and/or particular uses.

This problem is solved by the provision of the embodiments described in the claims.

Therefore, the present invention relates to nucleic acid molecules encoding a protein comprising the amino acid sequence indicated in Seq ID No. 6 or in Seq ID No. 8. Such proteins are present in the plastids of plant cells, bound to starch granules as well as in free, i.e. soluble form.

The present invention further relates to nucleic acid molecules comprising a sequence with the nucleotide sequence indicated in Seq ID No. 5 or in Seq ID No. 7, particularly the coding region indicated in Seq ID No. 5 or in Seq ID No. 7.

Nucleic acid molecules encoding a protein from maize, which in the plastids of the cells is partly granule-bound, and hybridizing to the above-mentioned nucleic acid molecules of the invention or their complementary strand are also the subject matter of the present invention. In this context the term "hybridization" signifies hybridization under conventional hybridizing conditions, preferably under stringent conditions as described for example in Sambrook et al., Molecular Cloning, A Laboratory Manual, 2nd Edition (1989) Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY).

More preferably hybridization occurs under the following conditions:

Hybridization buffer: 2 x SSC; 10 x Denhard's solution (Fikoll 400 + PEG + BSA; ratio 1:1:1); 0.1% SDS;
5 mM EDTA; 50 mM Na₂HPO₄; 250 µg/ml
herring sperm DNA; 50µg/ml tRNA; or
0.25 M sodiumphosphate buffer pH 7.2
1 mM EDTA
7% SDS

Hybridization temperature T = 65 + 68°C

Washing buffer: 0.2 x SSC; 0.1% SDS

Washing temperature T = 40 to 68°C.

Nucleic acid molecules hybridizing to the molecules according to the invention may be isolated e.g. from genomic or from cDNA libraries produced from maize cells or tissue.

The identification and isolation of such nucleic acid molecules may take place by using the molecules according to the invention or parts of these molecules or, as the case may be, the reverse complementary strands of these molecules, e.g. by hybridization according to standard methods (see e.g. Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, 2nd Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY).

As a probe for hybridization e.g. nucleic acid molecules may be used which exactly or basically contain the nucleotide sequence indicated under Seq ID No. 5 or under Seq ID No. 7 or parts thereof. The DNA fragments used as hybridization probe may also be synthetic DNA fragments which were produced by means of the conventional DNA synthesizing methods and the sequence of which is basically identical with that of a nucleic acid molecule of the invention. After identifying and isolating genes hybridizing to the nucleic acid sequences according to the invention, the sequence has to be determined and the properties of the proteins encoded by this sequence have to be analyzed.

Such hybridizing nucleic acid molecules also encompass fragments, derivatives and allelic variants of the above-mentioned nucleic acid molecules, which encode the above-mentioned protein. In this context fragments are described as parts of the nucleic acid molecules which are long enough in order to encode the above-described protein. The term derivative means that the sequences of these molecules differ from the sequences of the above-mentioned nucleic acid molecules at one or more positions and exhibit a high degree of

homology to the sequences of these molecules. Homology means a sequence identity of at least 40%, in particular an identity of at least 60%, preferably of more than 80% and still more preferably a sequence identity of more than 90% and particularly preferred of more than 95%. The deviations occurring when comparing with the above-described nucleic acid molecules might have been caused by addition, deletion, substitution, insertion or recombination.

Moreover, homology means that functional and/or structural equivalence exists between the respective nucleic acid molecules or the proteins they encode. The nucleic acid molecules, which are homologous to the above-described nucleic acid molecules and represent derivatives of these molecules, are generally variations of these nucleic acid molecules, that constitute modifications which exert the same biological function. These variations may be naturally occurring variations or mutations, whereby these mutations may have occurred naturally or they may have been introduced deliberately. Moreover the variations may be synthetically produced sequences.

The allelic variants may be naturally occurring as well as synthetically produced variants or variants produced by recombinant DNA techniques.

The proteins encoded by the various variants of the nucleic acid molecules according to the invention exhibit certain common characteristics. Enzyme activity, molecular weight, immunologic reactivity, conformation etc. may belong to these characteristics as well as physical properties such as the mobility in gel electrophoresis, chromatographic characteristics, sedimentation coefficients, solubility, spectroscopic properties, stability, pH-optimum, temperature-optimum etc.

Furthermore, the present invention relates to nucleic acid molecules the sequences of which, compared to the sequences of the above-mentioned molecules, are degenerated due to the genetic code and which encode a protein which is present in the plastids of plant cells partly in granule-bound and partly in free form, i.e. in a soluble form.

The nucleic acid molecules of the invention can, for example, be isolated from natural sources, produced by methods of genetic engineering, e.g. by PCR, or produced by means of synthesis methods known to the skilled person.

The nucleic acid molecules of the invention may be DNA molecules, such as cDNA or genomic DNA, as well as RNA molecules.

Furthermore, the invention relates to vectors, especially plasmids, cosmids, viruses, bacteriophages and other vectors common in genetic engineering, which contain the above-mentioned nucleic acid molecules of the invention.

In a preferred embodiment the nucleic acid molecules contained in the vectors are linked to regulatory elements that ensure the transcription and synthesis of a translatable RNA in prokaryotic and eukaryotic cells.

In a further embodiment the invention relates to host cells, in particular prokaryotic or eukaryotic cells, which have been transformed and/or recombinantly manipulated by an above-mentioned nucleic acid molecule of the invention or by a vector of the invention, as well as cells which are derived from such cells and which contain a nucleic acid molecule of the invention or a vector of the invention. This is preferably a bacterial cell or a plant cell.

It was now found that the protein encoded by the nucleic acid molecules of the invention influences the starch synthesis or modification and that changes in the amount of the protein in plant cells lead to changes in the starch metabolism of the plant, especially to the synthesis of starch with modified physical and chemical properties.

By providing the nucleic acid molecules of the invention it is possible to produce plants by means of recombinant DNA techniques synthesizing a modified starch which differs from the starch synthesized in wildtype plants with respect to its structure and its physical and chemical properties. For this purpose, the nucleic acid molecules of the invention are linked to regulatory elements, which ensure the transcription and translation in plant cells, and they are introduced into the plant cells.

Therefore, the present invention also relates to transgenic plant cells containing a nucleic acid molecule of the invention wherein the same is linked to regulatory elements which ensure the transcription in plant cells. The regulatory elements are preferably heterologous with respect to the nucleic acid molecule.

Such plant cells of the invention differ from naturally occurring plants among other things in that at least one copy of the nucleic acid molecule of the invention is integrated in their genome, possibly in addition to the naturally occurring copies. Furthermore, this/these additional copy/copies is/are integrated at a location in the genome at which they do not occur naturally. This may be proved, for example, by means of a Southern Blot analysis. Furthermore, such transgenic plant cells can preferably be distinguished from corresponding naturally occurring plant cells by at least one of the following features: If the nucleic acid molecule according to the invention, which was introduced into the plant cells, is

heterologous to the plant cells, the transgenic cells can be distinguished from non transformed cells due to the presence of transcripts from the introduced molecule according to the invention. Such transcripts can be detected, e.g., by Northern Blot analysis. Preferably the transgenic cells furthermore contain the protein encoded by the nucleic acid molecule according to the invention. The presence of the protein can be detected, e.g., by immunological methods such as Western Blot analysis.

If the nucleic acid molecule according to the invention which was introduced into the cells is homologous with respect to the cells, the transgenic cells can be distinguished from non-transformed cells, for example, due to the additional expression of the nucleic acid molecule according to the invention. In particular, the transgenic cells contain preferably more transcripts of the nucleic acid molecules according to the invention. This can be detected, e.g., by Northern Blot analysis. "More" preferably means at least 10% more, more preferably at least 20% more, and even more preferably at least 50% more. Accordingly, the transgenic cells contain preferably more protein according to the invention in comparison to non-transformed cells. This can be detected, e.g., by Western Blot analysis. Preferably, the cells contain at least 10% more protein according to the invention, more preferably at least 20% and even more preferably at least 50% more.

By means of methods known to the skilled person the transgenic plant cells can be regenerated to whole plants. The plants obtainable by regenerating the transgenic plant cells of the invention are also the subject-matter of the present invention.

A further subject-matter of the invention are plants which contain the above-described transgenic plant cells. The transgenic plants may in principle be plants of any desired

species, i.e. they may be monocotyledonous as well as dicotyledonous plants. These are preferably useful plants, in particular starch-synthesizing or starch-storing plants such as cereals (rye, barley, oats, wheat, millet, sago etc.), rice, maize, peas, wrinkled peas, cassava, potato, tomato, oil seed rape, soy bean, hemp, flax, sunflower, cow-pea and arrowroot.

The present invention also relates to a process for the production of a modified starch comprising the step of extracting from the above-described plants according to the invention and/or from starch storing parts of such plants the starch. Preferably, such a process furthermore comprises the steps of cultivating plants according to the invention and harvesting the cultivated plants and/or starch storing parts of these plants before the extraction of the starch.

Methods for extracting starch from plants or from starch storing parts of plants are well known to the person skilled in the art. Methods to extract starch from maize seeds are described, for example, in Eckhoff et al. (Cereal Chem. 73 (1996), 54-57). Extraction of maize starch on an industrial scale is normally achieved by "wet-milling". Furthermore, methods for the extraction of starch from various starch storing plants are described, for example, in Starch: Chemistry and Technology (eds.: Whistler, BeMiller and Paschall (1994) 2nd Edition, Academic Press Inc. London LTD; ISBN 0-12-746270-8; see e.g. Chapter XII, page 417-468: Corn and Sorghum Starches: Production; by Watson, S.A.; Chapter XIII, page 469-479: Tapioca, Arrowroot and Sago Starches: Production; by Corbishley and Miller; Chapter XIV, page 479-490: Potato Starch: Production and Uses; by Mitch; Chapter XV, page 491-506: Wheat starch: Production, Modification and Uses; by Knight and Olson; and Chapter XVI, page 507-528: Rice starch: Production and Uses; by Rohwer and Klem). Means usually used in

methods for the extraction of starches from plant materials are separators, decanters, hydroclones and different kinds of machines for drying the starch, e.g., spray drier or jet drier.

The present invention also relates to the starch obtainable from the transgenic plant cells and plants of the invention or by the above described process. Due to the expression or the additional expression of a nucleic acid molecule of the invention, the transgenic plant cells and plants of the invention synthesize a starch which is modified when compared to starch from wildtype-plants, i.e. non-transformed plants.

In particular, such a starch has preferably a higher phosphate content than starch synthesized by corresponding non-transformed cells or plants. A higher phosphate content preferably means that the starch contains at least 10% more phosphate, more preferably at least 30%, even more preferably at least 50% and particularly preferred at least 100% more phosphate than starch from corresponding non-transformed cells or plants. Starches with a high content of phosphate are, for example, of particular interest for the paper industry, e.g., for the preparation of the surface of paper. Normally, the paper industry uses chemically modified starch, for example, hydroxyethylated or phosphorylated starch, for the surface sizing or coating. The production of highly phosphorylated starch in plants would thus avoid the necessity to chemically modify starch in order to adapt it to the requirements of the paper industry.

A further subject-matter of the present invention is a method for the production of a protein which is present in plant cells in granule-bound form as well as in soluble form, in which host cells of the invention are cultivated under conditions that allow for the expression of the protein and in which the

protein is then isolated from the cultivated cells and/or the culture medium.

Furthermore, the invention relates to proteins encoded by the nucleic acid molecules of the invention as well as to proteins obtainable by the above-described method. These are preferably proteins from maize encoded by nuclear genes and which are localized in the plastids. In the plastids these enzymes are present in granule-bound as well as in free form.

A further subject-matter of the invention are antibodies which specifically recognize a protein of the invention. These may be monoclonal as well as polyclonal antibodies. Methods for the production of such antibodies are known to the skilled person.

Furthermore, the present invention relates to nucleic acid molecules specifically hybridizing with a nucleic acid molecule of the invention and exhibiting a length of at least 15 nucleotides. In this context specifically hybridizing signifies that under conventional hybridization conditions, preferably under stringent conditions, cross-hybridization with sequences encoding other proteins do not significantly occur. Such nucleic acid molecules preferably have a length of at least 20, more preferably a length of at least 50 and most preferably a length of at least 100 nucleotides. Such molecules can be used, for example, as PCR primers, as hybridization probes or as DNA molecules which encode antisense RNA.

Furthermore, it was found that it is possible to influence the properties of the starch synthesized in plant cells by reducing the amount of proteins encoded by the nucleic acid molecules according to the invention in the cells. This reduction may be effected, for example, by means of antisense expression of the

nucleic acid molecules of the invention, expression of suitable ribozymes or cosuppression.

Therefore, DNA molecules encoding an antisense RNA which is complementary to transcripts of a DNA molecule of the invention are also the subject-matter of the present invention, as well as these antisense molecules. Thereby, complementary does not signify that the encoded RNA has to be 100% complementary. A low degree of complementarity is sufficient, as long as it is high enough in order to inhibit the expression of a protein of the invention upon expression in plant cells. The transcribed RNA is preferably at least 90% and most preferably at least 95% complementary to the transcript of the nucleic acid molecule of the invention. In order to cause an antisense-effect during the transcription in plant cells such DNA molecules have a length of at least 15 bp, preferably a length of more than 100 bp and most preferably a length of more than 500 bp, however, usually less than 5000 bp, preferably shorter than 2500 bp.

The invention further relates to DNA molecules which, during expression in plant cells, lead to the synthesis of an RNA which in the plant cells due to a cosuppression-effect reduces the expression of the nucleic acid molecules of the invention encoding the described protein. The invention also relates to RNA molecules encoded thereby. The principle of the cosuppression as well as the production of corresponding DNA sequences is precisely described, for example, in WO 90/12084. Such DNA molecules preferably encode a RNA having a high degree of homology to transcripts of the nucleic acid molecules of the invention. It is, however, not absolutely necessary that the coding RNA is translatable into a protein.

In a further embodiment the present invention relates to DNA molecules encoding an RNA molecule with ribozyme activity which

specifically cleaves transcripts of a DNA molecule of the invention as well as these encoded RNA molecules.

Ribozymes are catalytically active RNA molecules capable of cleaving RNA molecules and specific target sequences. By means of recombinant DNA techniques it is possible to alter the specificity of ribozymes. There are various classes of ribozymes. For practical applications aiming at the specific cleavage of the transcript of a certain gene, use is preferably made of representatives of two different groups of ribozymes. The first group is made up of ribozymes which belong to the group I intron ribozyme type. The second group consists of ribozymes which as a characteristic structural feature exhibit the so-called "hammerhead" motif. The specific recognition of the target RNA molecule may be modified by altering the sequences flanking this motif. By base pairing with sequences in the target molecule these sequences determine the position at which the catalytic reaction and therefore the cleavage of the target molecule takes place. Since the sequence requirements for an efficient cleavage are low, it is in principle possible to develop specific ribozymes for practically each desired RNA molecule.

In order to produce DNA molecules encoding a ribozyme which specifically cleaves transcripts of a DNA molecule of the invention, for example a DNA sequence encoding a catalytic domain of a ribozyme is bilaterally linked with DNA sequences which are homologous to sequences of the target enzyme. Sequences encoding the catalytic domain may for example be the catalytic domains of the satellite DNA of the SCMo virus (Davies et al., Virology 177 (1990), 216-224) or that of the satellite DNA of the TobR virus (Steinecke et al., EMBO J. 11 (1992), 1525-1530; Haseloff and Gerlach, Nature 334 (1988), 585-591). The DNA sequences flanking the catalytic domain are preferably derived from the above-described DNA molecules of the invention.

In a further embodiment the present invention relates to vectors containing the above-described DNA molecules, in particular those in which the described DNA molecules are linked with regulatory elements ensuring the transcription in plant cells.

Furthermore, the present invention relates to host cells containing the described DNA molecules or vectors. The host cell may be a prokaryotic cell, such as a bacterial cell, or a eukaryotic cell. The eukaryotic host cells are preferably plant cells.

Furthermore, the invention relates to transgenic plant cells containing an above-described DNA molecule encoding an antisense-RNA, a ribozyme or an RNA which leads to a cosuppression effect, whereby the DNA molecule is linked to DNA elements ensuring the transcription in plant cells. These transgenic plant cells may be regenerated to whole plants according to well-known techniques. Thus, the invention also relates to plants which may be obtained through regeneration from the described transgenic plant cells, as well as to plants containing the described transgenic plant cells. The transgenic plants themselves may be plants of any desired plant species, preferably useful plants, particularly starch-storing ones, as indicated above, and most preferably maize plant cells.

Furthermore, the invention relates to the antisense RNA molecules encoded by the described DNA molecules, as well as to RNA molecules with ribozyme activity and RNA molecules which lead to a cosuppression effect which are obtainable, for example, by means of transcription.

A further subject-matter of the invention is a method for the production of transgenic plant cells, which in comparison to

non-transformed cells synthesize a modified starch. In this method the amount of proteins encoded by the DNA molecules of the invention, which are present in the cells in endogenic form, is reduced in the plant cells.

In a preferred embodiment this reduction is effected by means of an antisense effect. For this purpose the DNA molecules of the invention or parts thereof are linked in antisense orientation with a promoter ensuring the transcription in plant cells and possibly with a termination signal ensuring the termination of the transcription as well as the polyadenylation of the transcript. In order to ensure an efficient antisense effect in the plant cells the synthesized antisense RNA should exhibit a minimum length of 15 nucleotides, preferably of at least 100 nucleotides and most preferably of at least 500 nucleotides. Furthermore, the DNA sequence encoding the antisense RNA should be homologous with respect to the plant species to be transformed. However, DNA sequences exhibiting a high degree of homology to DNA sequences which are present in the cells in endogenic form may also be used, preferably with an homology of more than 90% and most preferably with an homology of more than 95%.

In a further embodiment the reduction of the amount of proteins encoded by the DNA molecules of the invention is effected by a ribozyme effect. The basic effect of ribozymes as well as the construction of DNA molecules encoding such RNA molecules have already been described above. In order to express an RNA with ribozyme activity in transgenic cells the above described DNA molecules encoding a ribozyme are linked with DNA elements which ensure the transcription in plant cells, particularly with a promoter and a termination signal. The ribozymes synthesized in the plant cells lead to the cleavage of

transcripts of DNA molecules of the invention which are present in the plant cells in endogenic form.

A further possibility in order to reduce the amount of proteins encoded by the nucleic acid molecules of the invention is cosuppression. Therefore, the plant cells obtainable by the method of the invention are a further subject matter. These plant cells are characterized in that their amount of proteins encoded by the DNA molecules of the invention is reduced and that in comparison to wildtype cells they synthesize a modified starch.

Preferably, the transgenic cells show a reduction in the amount of transcripts encoding a protein according to the present invention of at least 30%, more preferably of at least 50%, even more preferably of at least 70% and most preferably of at least 90% in comparison to corresponding non-transformed cells. The amount of transcripts can be determined, for example, by Northern Blot analysis. Furthermore, the cells preferably show a corresponding reduction of the amount of the protein according to the invention. This can be determined, for example, by immunological methods such as Western Blot analysis.

In a particularly preferred embodiment of the present invention not only the synthesis of a protein of the invention is reduced in the transformed plant cells, but moreover also the synthesis of at least one further enzyme involved in starch synthesis and/or modification. In this context, for example, starch granule-bound starch synthases or branching enzymes are preferred.

Furthermore, the invention relates to plants obtainable by regeneration of the described plant cells as well as to plants containing the described cells of the invention.

The present invention also relates to a process for the production of a modified starch comprising the step of extracting from the above-described plants according to the invention and/or from starch storing parts of such plants the starch. Preferably, such a process furthermore comprises the steps of cultivating plants according to the invention; and harvesting the cultivated plants and/or starch storing parts of these plants before the extraction of the starch.

The present invention also relates to the starch obtainable from the described transgenic plant cells and plants or obtainable by the above described process. Due to the expression of the described DNA molecules encoding antisense RNA, a ribozyme or a cosuppression RNA in the transgenic plant cells the amount of proteins encoded by the DNA molecules of the invention which are present in the cells in endogenic form, is reduced. Surprisingly, this reduction leads to a drastic change of the physical and chemical properties of the starch synthesized in the plant cells. When compared to starch from non-transformed cells or plants the modified starch preferably exhibits altered pastification properties, i.e. an altered viscosity of the watery solutions of the starch and/or an altered, in particular a reduced phosphate content.

The expression of the nucleic acid molecules of the invention may in principle take place in any kind of plant species. Monocotyledonous and dicotyledonous plants are preferred, in particular useful plants and preferably starch-storing plants such as cereals (rye, barley, oats, wheat, millet, sago etc.), rice, maize, peas, wrinkled peas, cassava, potato, tomato,

oilseed rape, soy bean, hemp, flax, sunflower, cow-pea and arrowroot.

Within the framework of the present invention the term "regulatory DNA elements ensuring the transcription in plant cells" are DNA regions which allow for the initiation or the termination of transcription in plant cells. DNA regions ensuring the initiation of transcription are in particular promoters.

For the expression of the various above-described DNA molecules of the invention in plants any promoter functioning in plant cells may be used. The promoter may be homologous or heterologous with respect to the used plant species. Use may, for example, be made of the 35S promoter of the cauliflower mosaic virus (Odell et al., Nature 313 (1985), 810-812) which ensures a constitutive expression in all plant tissues and also of the promoter construct described in WO/9401571. However, use may also be made of promoters which lead to an expression of subsequent sequences only at a point of time determined by exogenous factors (such as in WO/9307279) or in a particular tissue of the plant (see e.g. Stockhaus et al., EMBO J. 8 (1989), 2245-2251). Promoters which are active in the starch-storing parts of the plant to be transformed are preferably used. In the case of maize these parts are the maize seeds, in the case of potatoes the tubers. In order to transform potatoes the tuber-specific B33-promoter (Rocha-Sosa et al., EMBO J. 8 (1989), 23-29) may be used particularly, but not exclusively. Apart from promoters, DNA regions initiating transcription may also contain DNA sequences ensuring a further increase of transcription, such as the so-called enhancer-elements.

Furthermore, the term "regulatory DNA elements" may also comprise termination signals which serve to correctly end the transcription and to add a poly-A-tail to the transcript which is believed to stabilize the transcripts. Such elements are

described in the literature and can be exchanged as desired. Examples for such termination sequences are the 3'-nontranslatable regions comprising the polyadenylation signal of the nopaline synthase gene (NOS gene) or the octopine synthase gene (Gielen et al., EMBO J. 8 (1989), 23-29) from agrobacteria, or the 3'-nontranslatable regions of the genes of the storage proteins from soy bean as well as the genes of the small subunit of ribulose-1,5-biphosphate-carboxylase (ssRUBISCO).

The introduction of the DNA molecules of the invention into plant cells is preferably carried out using plasmids. Plasmids ensuring a stable integration of the DNA into the plant genome are preferred.

In order to prepare the introduction of foreign genes in higher plants a large number of cloning vectors are at disposal, containing a replication signal for E.coli and a marker gene for the selection of transformed bacterial cells. Examples for such vectors are pBR322, pUC series, M13mp series, pACYC184 etc. The desired sequence may be integrated into the vector at a suitable restriction site. The obtained plasmid is used for the transformation of E.coli cells. Transformed E.coli cells are cultivated in a suitable medium and subsequently harvested and lysed. The plasmid is recovered by means of standard methods. As an analyzing method for the characterization of the obtained plasmid DNA use is generally made of restriction analysis and sequence analysis. After each manipulation the plasmid DNA may be cleaved and the obtained DNA fragments may be linked to other DNA sequences.

In order to introduce DNA into plant host cells a wide range of techniques are at disposal. These techniques comprise the transformation of plant cells with T-DNA by using *Agrobacterium tumefaciens* or *Agrobacterium rhizogenes* as transformation medium, the fusion of protoplasts, the injection and the

electroporation of DNA, the introduction of DNA by means of the biolistic method as well as further possibilities.

In the case of injection and electroporation of DNA into plant cells, there are no special demands made to the plasmids used. Simple plasmids such as pUC derivatives may be used. However, in case that whole plants are to be regenerated from cells transformed in such a way, a selectable marker gene should be present.

Depending on the method of introducing desired genes into the plant cell, further DNA sequences may be necessary. If the Ti- or Ri-plasmid is used e.g. for the transformation of the plant cell, at least the right border, more frequently, however, the right and left border of the Ti- and Ri-plasmid T-DNA has to be connected to the foreign gene to be introduced as a flanking region.

If *Agrobacteria* are used for transformation, the DNA which is to be introduced must be cloned into special plasmids, namely either into an intermediate vector or into a binary vector. Due to sequences homologous to the sequences within the T-DNA, the intermediate vectors may be integrated into the Ti- or Ri-plasmid of the *Agrobacterium* due to homologous recombination. This also contains the *vir*-region necessary for the transfer of the T-DNA. Intermediate vectors cannot replicate in *Agrobacteria*. By means of a helper plasmid the intermediate vector may be transferred to *Agrobacterium tumefaciens* (conjugation). Binary vectors may replicate in *E. coli* as well as in *Agrobacteria*. They contain a selectable marker gene as well as a linker or polylinker which is framed by the right and the left T-DNA border region. They may be transformed directly into the *Agrobacteria* (Holsters et al. *Mol. Gen. Genet.* 163 (1978), 181-187). The plasmids used for the transformation of the *Agrobacteria* further comprise a selectable marker gene, such as the NPT II gene which allows for selecting transformed bacteria. The *Agrobacterium* acting as host cell should contain

a plasmid carrying a vir-region. The vir-region is necessary for the transfer of the T-DNA into the plant cell. Additional T-DNA may be present. The Agrobacterium transformed in such a way is used for the transformation of plant cells.

The use of T-DNA for the transformation of plant cells was investigated intensely and described sufficiently in EP 120 516; Hoekema, In: The Binary Plant Vector System Offsetdrukkerij Kanters B.V., Alblasterdam (1985), Chapter V; Fraley et al., Crit. Rev. Plant. Sci., 4, 1-46 and An et al. EMBO J. 4 (1985), 277-287. Some binary vectors may already be obtained commercially, such as pBIN19 (Clontech Laboratories, Inc., USA).

For transferring the DNA into the plant cells, plant explants may suitably be co-cultivated with Agrobacterium tumefaciens or Agrobacterium rhizogenes. From the infected plant material (e.g. pieces of leaves, stem segments, roots, but also protoplasts or suspension-cultivated plant cells) whole plants may then be regenerated in a suitable medium which may contain antibiotics or biozides for the selection of transformed cells. The plants obtained in such a way may then be examined as to whether the introduced DNA is present or not. Other possibilities in order to introduce foreign DNA by using the biolistic method or by transforming protoplasts are known to the skilled person (cf. e.g. Willmitzer, L., 1993 Transgenic plants. In: Biotechnology, A Multi-Volume Comprehensive Treatise (H.J. Rehm, G. Reed, A. Pühler, P. Stadler, editors), Vol. 2, 627-659, VCH Weinheim-New York-Basel-Cambridge).

Whereas the transformation of dicotyledonous plants by Ti-plasmid-vector systems by means of Agrobacterium tumefaciens is a well-established method, more recent studies indicate that the transformation with vectors based on Agrobacterium can also be used in the case of monocotyledonous plants (Chan et al.,

Plant Mol. Biol. 22 (1993), 491-506; Hiei et al., Plant J. 6 (1994), 271-282).

Alternative systems for the transformation of monocotyledonous plants are the transformation by means of the biolistic approach, protoplast transformation, electroporation of partially permeabilized cells, the introduction of DNA by means of glass fibers.

There are various references in the relevant literature dealing specifically with the transformation of maize (cf. e.g. WO95/06128, EP 0 513 849; EP 0 465 875). In EP 292 435 a method is described by means of which fertile plants may be obtained starting from mucousless, friable granulous maize callus. In this context it was furthermore observed by Shillito et al. (Bio/Technology 7 (1989), 581) that for regenerating fertile plants it is necessary to start from callus-suspension cultures from which a culture of dividing protoplasts can be produced which is capable to regenerate to plants. After an in vitro cultivation period of 7 to 8 months Shillito et al. obtain plants with viable descendants which, however, exhibited abnormalities in morphology and reproductivity.

Prioli and Söndahl (Bio/Technology 7 (1989), 589) have described how to regenerate and to obtain fertile plants from maize protoplasts of the Cateto maize inbreed Cat 100-1. The authors assume that the regeneration of protoplast to fertile plants depends on a number of various factors such as the genotype, the physiological state of the donor-cell and the cultivation conditions. Once the introduced DNA has been integrated in the genome of the plant cell, it usually continues to be stable there and also remains within the descendants of the originally transformed cell. It usually contains a selectable marker which confers resistance against biozides or against an antibiotic such as kanamycin, G 418, bleomycin, hygromycin or phosphinotricine etc. to the transformed plant cells. The individually selected marker

should therefore allow for a selection of transformed cells against cells lacking the introduced DNA.

The transformed cells grow in the usual way within the plant (see also McCormick et al., Plant Cell Reports 5 (1986), 81-84). The resulting plants can be cultivated in the usual way and cross-bred with plants having the same transformed genetic heritage or another genetic heritage. The resulting hybrid individuals have the corresponding phenotypic properties.

Two or more generations should be grown in order to ensure whether the phenotypic feature is kept stably and whether it is transferred. Furthermore, seeds should be harvested in order to ensure that the corresponding phenotype or other properties will remain.

Due to its properties the starch obtained from the plant cells or from the plants of the invention or obtainable by the processes of the invention is not only suitable for the specific purposes already mentioned herein, but also for various industrial uses.

Basically, starch can be subdivided into two major fields. One field comprises the hydrolysis products of starch and the so-called native starches. The hydrolysis products essentially comprise glucose and glucans components obtained by enzymatic or chemical processes. They can be used for further processes, such as fermentation and chemical modifications. In this context, it might be of importance that the hydrolysis process can be carried out simply and inexpensively. Currently, it is carried out substantially enzymatically using amyloglucosidase. It is thinkable that costs might be reduced by using lower amounts of enzymes for hydrolysis due to changes in the starch structure, e.g. increasing the surface of the grain, improved digestibility due to less branching or a steric structure, which limits the accessibility for the used enzymes.

The use of the so-called native starch which is used because of its polymer structure can be subdivided into two further areas:

(a) Use in foodstuffs

Starch is a classic additive for various foodstuffs, in which it essentially serves the purpose of binding aqueous additives and/or causes an increased viscosity or an increased gel formation. Important characteristic properties are flowing and sorption behavior, swelling and pastification temperature, viscosity and thickening performance, solubility of the starch, transparency and paste structure, heat, shear and acid resistance, tendency to retrogradation, capability of film formation, resistance to freezing/thawing, digestibility as well as the capability of complex formation with e.g. inorganic or organic ions.

(b) Use in non-foodstuffs

The other major field of application is the use of starch as an adjuvant in various production processes or as an additive in technical products. The major fields of application for the use of starch as an adjuvant are, first of all, the paper and cardboard industry. In this field, the starch is mainly used for retention (holding back solids), for sizing filler and fine particles, as solidifying substance and for dehydration. In addition, the advantageous properties of starch with regard to stiffness, hardness, sound, grip, gloss, smoothness, tear strength as well as the surfaces are utilized.

Within the paper production process, a differentiation can be made between four fields of application, namely surface, coating, mass and spraying.

The requirements on starch with regard to surface treatment are essentially a high degree of brightness, corresponding viscosity, high viscosity stability, good

film formation as well as low formation of dust. When used in coating the solid content, a corresponding viscosity, a high capability to bind as well as a high pigment affinity play an important role. As an additive to the mass rapid, uniform, loss-free dispersion, high mechanical stability and complete retention in the paper pulp are of importance. When using the starch in spraying, corresponding content of solids, high viscosity as well as high capability to bind are also significant.

A major field of application is, for instance, in the adhesive industry, where the fields of application are subdivided into four areas: the use as pure starch glue, the use in starch glues prepared with special chemicals, the use of starch as an additive to synthetic resins and polymer dispersions as well as the use of starches as extenders for synthetic adhesives. 90% of all starch-based adhesives are used in the production of corrugated board, paper sacks and bags, composite materials for paper and aluminum, boxes and wetting glue for envelopes, stamps, etc.

Another possible use as adjuvant and additive is in the production of textiles and textile care products. Within the textile industry, a differentiation can be made between the following four fields of application: the use of starch as a sizing agent, i.e. as an adjuvant for smoothing and strengthening the burring behavior for the protection against tensile forces active in weaving as well as for the increase of wear resistance during weaving, as an agent for textile improvement mainly after quality-deteriorating pretreatments, such as bleaching, dying, etc., as thickener in the production of dye pastes for the prevention of dye diffusion and as an additive for warping agents for sewing yarns.

Furthermore, starch may be used as an additive in building materials. One example is the production of gypsum plaster boards, in which the starch mixed in the thin plaster pastifies with the water, diffuses at the surface of the gypsum board and thus binds the cardboard to the board. Other fields of application are admixing it to plaster and mineral fibers. In ready-mixed concrete, starch may be used for the deceleration of the sizing process.

Furthermore, the starch is advantageous for the production of means for ground stabilization used for the temporary protection of ground particles against water in artificial earth shifting. According to state-of-the-art knowledge, combination products consisting of starch and polymer emulsions can be considered to have the same erosion- and encrustation-reducing effect as the products used so far; however, they are considerably less expensive.

Another field of application is the use of starch in plant protectives for the modification of the specific properties of these preparations. For instance, starches are used for improving the wetting of plant protectives and fertilizers, for the dosed release of the active ingredients, for the conversion of liquid, volatile and/or odorous active ingredients into microcrystalline, stable, deformable substances, for mixing incompatible compositions and for the prolongation of the duration of the effect due to a reduced disintegration.

Starch may also be used in the fields of drugs, medicine and in the cosmetics industry. In the pharmaceutical industry, the starch may be used as a binder for tablets or for the dilution of the binder in capsules. Furthermore, starch is suitable as disintegrant for tablets since, upon swallowing, it absorbs fluid and after a short time it swells so much that the active ingredient is released. For qualitative reasons, medicinal flowance

and dusting powders are further fields of application. In the field of cosmetics, the starch may for example be used as a carrier of powder additives, such as scents and salicylic acid. A relatively extensive field of application for the starch is toothpaste.

The use of starch as an additive in coal and briquettes is also thinkable. By adding starch, coal can be quantitatively agglomerated and/or briquetted in high quality, thus preventing premature disintegration of the briquettes. Barbecue coal contains between 4 and 6% added starch, calorated coal between 0.1 and 0.5%. Furthermore, the starch is suitable as a binding agent since adding it to coal and briquette can considerably reduce the emission of toxic substances.

Furthermore, the starch may be used as a flocculant in the processing of ore and coal slurry.

Another field of application is the use as an additive to process materials in casting. For various casting processes cores produced from sands mixed with binding agents are needed. Nowadays, the most commonly used binding agent is bentonite mixed with modified starches, mostly swelling starches.

The purpose of adding starch is increased flow resistance as well as improved binding strength. Moreover, swelling starches may fulfill more prerequisites for the production process, such as dispersability in cold water, rehydratisability, good mixability in sand and high capability of binding water.

In the rubber industry starch may be used for improving the technical and optical quality. Reasons for this are improved surface gloss, grip and appearance. For this purpose, the starch is dispersed on the sticky rubberized surfaces of rubber substances before the cold

vulcanization. It may also be used for improving the printability of rubber.

Another field of application for the modified starch is the production of leather substitutes.

In the plastics market the following fields of application are emerging: the integration of products derived from starch into the processing process (starch is only a filler, there is no direct bond between synthetic polymer and starch) or, alternatively, the integration of products derived from starch into the production of polymers (starch and polymer form a stable bond).

The use of the starch as a pure filler cannot compete with other substances such as talcum. This situation is different when the specific starch properties become effective and the property profile of the end products is thus clearly changed. One example is the use of starch products in the processing of thermoplastic materials, such as polyethylene. Thereby, starch and the synthetic polymer are combined in a ratio of 1 : 1 by means of coexpression to form a 'master batch', from which various products are produced by means of common techniques using granulated polyethylene. The integration of starch in polyethylene films may cause an increased substance permeability in hollow bodies, improved water vapor permeability, improved antistatic behavior, improved anti-block behavior as well as improved printability with aqueous dyes.

Another possibility is the use of the starch in polyurethane foams. Due to the adaptation of starch derivatives as well as due to the optimization of processing techniques, it is possible to specifically control the reaction between synthetic polymers and the starch's hydroxy groups. The results are polyurethane films having the following property profiles due to the use of starch: a reduced coefficient of thermal expansion, decreased shrinking behavior, improved pressure/tension behavior, increased water vapor permeability

without a change in water acceptance, reduced flammability and cracking density, no drop off of combustible parts, no halides and reduced aging. Disadvantages that presently still exist are reduced pressure and impact strength.

Product development of film is not the only option. Also solid plastics products, such as pots, plates and bowls can be produced by means of a starch content of more than 50%. Furthermore, the starch/polymer mixtures offer the advantage that they are much easier biodegradable.

Furthermore, due to their extreme capability to bind water, starch graft polymers have gained utmost importance. These are products having a backbone of starch and a side lattice of a synthetic monomer grafted on according to the principle of radical chain mechanism. The starch graft polymers available nowadays are characterized by an improved binding and retaining capability of up to 1000 g water per g starch at a high viscosity. These super absorbers are used mainly in the hygiene field, e.g. in products such as diapers and sheets, as well as in the agricultural sector, e.g. in seed pellets.

What is decisive for the use of the new starch modified by recombinant DNA techniques are, on the one hand, structure, water content, protein content, lipid content, fiber content, ashes/phosphate content, amylose/amylopectin ratio, distribution of the relative molar mass, degree of branching, granule size and shape as well as crystallization, and on the other hand, the properties resulting in the following features: flow and sorption behavior, pastification temperature, viscosity, thickening performance, solubility, paste structure, transparency, heat, shear and acid resistance, tendency to retrogradation, capability of gel formation, resistance to freezing/thawing, capability of complex formation, iodine binding, film formation, adhesive strength, enzyme stability,

digestibility and reactivity. The most remarkable feature is viscosity.

Moreover, the modified starch obtained from the plant cells of the invention may be subjected to further chemical modification, which will result in further improvement of the quality for certain of the above-described fields of application. These chemical modifications are principally known to the person skilled in the art. These are particularly modifications by means of

- acid treatment
- oxidation and
- esterification (formation of phosphate, nitrate, sulphate, xanthate, acetate and citrate starches. Further organic acids may also be used for esterification.)
- formation of starch ethers (starch alkyl ether, O-allyl ether, hydroxylalkyl ether, O-carboxymethyl ether, N-containing starch ethers, S-containing starch ethers)
- formation of branched starches
- formation of starch graft polymers.

The invention also relates to propagation material of the plants of the invention, such as seeds, fruits, cuttings, tubers or root stocks, wherein this propagation material contains plant cells of the invention.

Deposits

The plasmids produced and/or used within the framework of the present invention have been deposited at the internationally acknowledged deposit "Deutsche Sammlung von Mikroorganismen (DSM)" in Braunschweig, Federal Republic of Germany, according to the requirements of the Budapest treaty for international acknowledgment of microorganism deposits for patenting (deposit number; deposition date):

plasmid pBinAR Hyg	(DSM 9505)	(10/20/94)
plasmid p33-anti-BE	(DSM 6146)	(08/20/90)
plasmid pRL2	(DSM 10225)	(09/04/95)

Description of the figures

Fig. 1 shows the plasmid p35S-anti-RL.

Plasmid structure:

A = fragment A: CaMV 35S promoter, nt 6909-7437 (Franck et al., Cell 21 (1980), 285-294)

B = fragment B: Asp718 fragment from pRL1 with a length of approximately 1949 bp

Orientation relative to the promoter: anti-sense

The arrow indicates the direction of the open reading frame.

C = fragment C: nt 11748-11939 of the T-DNA of Ti-plasmid pTiACH5 T-DNA (Gielen et al., EMBO J. 3 (1984), 835-846)

Fig. 2 shows the plasmid pB33-anti-RL

Plasmid structure:

A = fragment A: B33 promoter of the patatin gene B33 from *Solanum tuberosum* (Rocha-Sosa et al., EMBO J. 8 (1989), 23-29)

B = fragment B: Asp718 fragment from pRL1 with a length of approximately 1949 bp

Orientation relative to the promoter: anti-sense

The arrow indicates the direction of the open reading frame.

C = fragment C: nt 11748-11939 of the T-DNA of Ti-plasmid pTiACH5 T-DNA (Gielen et al., EMBO J. 3 (1984), 835-846)

Fig. 3 shows a Brabender curve of a watery starch solution, recorded with a Viskograph-E-type Brabender viscograph, which was isolated from non-transformed potato plants of the variety Désirée (see also Example 8).

Thereby signifying:	Drehm.	torque
	[BE]	Brabender unit
	Temp.	temperature
	A	start of pastification
	B	maximum degree of viscosity
	C	start of the 96°C-period.....
	D	start of cooling-off period
	E	end of cooling-off period
	F	end of the end-50°C period

The blue line indicates the viscosity; the red line stands for temperature.

Fig. 4 shows a Brabender curve of a watery starch solution, recorded with a Viskograph-E-type Brabender viscograph, which was isolated from potato plants transformed with the plasmid p35S-anti-RL (see also Example 8). For the meaning of the abbreviations see Figure 3.

Fig. 5 shows a Brabender curve of a watery solution of starch from potatoes transformed with the plasmid pB33-anti-RL (see also Example 8), recorded with a Viskograph-E-type Brabender viscograph. For the meaning of the abbreviations see Figure 3.

Fig. 6 shows curves of watery solutions of starch isolated from potato plants (see also Example 12), which were recorded with a Rapid Visco Analyser. The red line stands for the temperature; the blue lines 1, 2, 3 and 4 show the viscosities of the following starch solutions:

- Line 1: starch isolated from wildtype plants,
- Line 2: starch isolated from plants in which only the branching enzyme was inhibited (cf. Example 1 of patent application WO92/14827),
- Line 3: starch isolated from plants in which merely the concentration of the proteins of the invention had been reduced (cf. Example 6).
- Line 4: starch isolated from plants which had been transformed with the plasmid p35S-anti-RL in combination with the p35SH-anti-BE plasmid (cf. Example 12).

Fig. 7 shows curves of watery solutions of starch isolated from potato plants (see also Example 13), which were recorded with a Rapid Visco Analyser. The red line stands for the temperature; the blue lines 1, 2, 3 and 4 show the viscosities of the following starch solutions:

- Line 1: starch isolated from wildtype plants,
- Line 2: starch isolated from plants which had solely been transformed with the plasmid pB33-anti-GBSSI (so-called waxy-potato),
- Line 3: starch isolated from plants which had been solely transformed with the plasmid p35S-anti-RL (cf. Example 6).
- Line 4: starch isolated from plants which had been transformed with the plasmid pB33-anti-RL in combination with the plasmid pB33-anti-GBSSI (cf. Example 13).

Fig. 8 shows the pRL2 plasmid which comprises a full-length cDNA from potato encoding an R1 enzyme.

The Examples illustrate the invention.

Used media and solutions

Elution buffer:	25 mM Tris pH 8,3 250 mM glycine
Dialysis buffer:	50 mM Tris-HCl pH 7,0 50 mM NaCl 2 mM EDTA 14,7 mM β -mercaptoethanol 0,5 mM PMSF
Protein buffer:	50 mM sodium phosphate buffer pH 7,2 10 mM EDTA 0,5 mM PMSF 14,7 mM β -mercaptoethanol
Lugol solution:	12 g KI 6 g I ₂ ad 1,8 l with ddH ₂ O
20 x SSC:	175.3 g NaCl 88.2 g sodium citrate ad 1000 ml with ddH ₂ O ph 7,0 with 10 N NaOH
10 x MEN:	200 mM MOPS 50 mM sodium acetate 10 mM EDTA pH 7,0
NSEB buffer:	0,25 M sodium phosphate buffer pH 7,2 7% SDS

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1 mM EDTA

1% BSA (w/v)

YT 8 g Bacto-Yeast extract
 5 g Bacto-Tryptone
 5 g NaCl
 ad 1000 ml with ddH₂O

Protoplast isolation medium (100 ml)

Cellulase Onozuka R S (Meiji Seika, Japan)	800 mg
Pectolyase Y 23	40 mg
KNO ₃	200 mg
KH ₂ PO ₄	136 mg
K ₂ HPO ₄	47 mg
CaCl ₂ 2H ₂ O	147 mg
MgSO ₄ 7H ₂ O	250 mg
Bovine serum albumine (BSA)	20 mg
Glucose	4000 mg
Fructose	4000 mg
Sucrose	1000 mg
pH	5,8
Osmolarity	660 mosm.

Protoplast washing solution 1: like protoplast isolating solution, but without cellulase, pectolyase and BSA

Transformation buffers:

a) Glucose	0,5 M
MES	0,1 %
MgCl ₂ 6H ₂ O	25 mM
pH	5,8
adjust to 600 mosm.	

b) PEG 6000-solution

Glucose	0,5 M
MgCl ₂ 6H ₂ O	100 mM
Hepes	20 mM
pH	6,5

PEG 6000 is added to the buffer described in b) immediately prior to the use of the solution (40 % w/v PEG). The solution is filtered with a 0,45 µm sterile filter.

W5 solution

CaCl ₂	125 mM
NaCl	150 mM
KCl	5 mM
Glucose	50 mM

Protoplast culture medium (indicated in mg/l)

KNO ₃	3000
(NH ₄) ₂ SO ₄	500
MgSO ₄ 7H ₂ O	350
KH ₂ PO ₄	400
CaCl ₂ 2H ₂ O	300

Fe-EDTA and trace elements as in the Murashige-Skoog medium (Physiol. Plant, 15 (1962), 473).

m-inosite	100
Thiamine HCl	1,0
Nicotine acid amide	0,5
Pyridoxine HCl	0,5
Glycine	2,0
Glucuronic acid	750
Galacturonic acid	750

Galactose	500
Maltose	500
Glucose	36.000
Fructose	36.000
Sucrose	30.000
Asparagine	500
Glutamine	100
Proline	300
Caseinhydrolysate	500
2,4 dichlorophenoxy acetic acid (2,4-D)	0,5
pH	5,8
Osmolarity	600 mosm.

Buffer A	2x	SSC
	10x	Denhardts solution
	0,1 %	SDS
	5 mM	EDTA
	50 mM	disodium phosphate
	250 µg/ml	herring sperm DNA

In the example the following standard methods were used:

1. Cloning

For cloning in E.coli the vector pBluescriptSK was used.

For plant transformation the gene constructs were cloned into the binary vector pBinAR (Höfgen and Willmitzer, Plant Sci. 66 (1990), 221-230) and B33-Hyg.

2. Bacterial strains

For the Bluescript vector and for the pBinAR and B33-Hyg constructs use was made of the E.coli strain DH5 α (Bethesda Research Laboratories, Gaithersburgh, USA).

The transformation of plasmid in potato plants was carried out by means of the *Agrobacterium tumefaciens* strain C58C1 pGV2260 (Deblaere et al., Nucl. Acids Res. 13 (1985), 4777:4788).

3. Transformation of *Agrobacterium tumefaciens*

The DNA transfer was carried out by means of direct transformation according to the method of Höfgen & Willmitzer (Nucleic Acids Res. 16 (1988), 9877). The plasmid DNA of transformed *Agrobacteria* was isolated according to the method of Birnboim & Doly (Nucleic Acids Res. 7 (1979), 1513-1523) and electrophoretically analyzed after suitable restriction cleavage.

4. Transformation of potatoes

Ten small leaves of a sterile potato culture (*Solanum tuberosum* L. cv. Désirée) injured by a scalpel were treated with 10 ml MS medium (Murashige & Skoog, Physiol. Plant. 15 (1962), 473-497) with 2% sucrose. The medium contained 50 μ l of a *Agrobacterium tumefaciens* overnight-culture grown under selection. After slightly shaking it for 3-5 minutes, another incubation took place in darkness for two days. The leaves were subsequently put on MS medium with 1,6% glucose, 5 mg/l naphthyle acetic acid, 0,2 mg/l benzylaminopurine, 250 mg/l claforan, 50 mg/l kanamycin or 1 mg/l hygromycin B, and 0,80% Bacto Agar for

callus induction. After a one-week incubation at 25°C and 3000 lux the leaves were put on MS-medium with 1,6% glucose, 1,4 mg/l zeatine ribose, 20 mg/l naphthyle acetic acid, 20 mg/l giberellic acid, 250 mg/l claforan, 50 mg/l kanamycin or 3 mg/l hygromycin B and 0,80% Bacto Agar for shoot induction.

5. Transformation of maize

(a) Production of protoplasts of the cell line DSM 6009

Protoplast isolation

2-4 days, preferably 3 days after the last change of medium in a protoplast suspension culture the liquid medium is pumped off and the remaining cells are washed in 50 ml protoplast washing solution 1 and sucked dry once more. 10 ml protoplast isolation medium are added to 2 g of harvested cell mass. The resuspended cells and cell aggregates are incubated at $27 \pm 2^\circ\text{C}$ for 4 to 6 hours in the darkness, while shaking it slightly (at 30 to 40 rpm).

Protoplast purification

As soon as the release of at least 1 million protoplasts/ml has taken place (microscopic inspection), the suspension is sifted through a stainless steel or nylon sieve with a mesh size of 200 or 45 μm . The combination of a 100 μm and a 60 μm sieve allows for separating the cell aggregates just as well. The protoplast-containing filtrate is examined microscopically. It usually contains 98 - 99% protoplasts. The rest are undigested single cells. Protoplast preparations with such a degree of

purity are used for transformation experiments without additional gradient centrifugation. The protoplasts are sedimented by means of centrifugation (100 UpM in the swing-out rotor (100 x g, 3 minutes)). The supernatant is abandoned and the protoplasts are resuspended in washing solution 1. The centrifugation is repeated and the protoplasts are subsequently resuspended in the transformation buffer.

(b) Protoplast transformation

The protoplasts resuspended in the transformation buffer are filled in 10 ml portions into 50 ml polyallomer tubes at a titer of $0.5 - 1 \times 10^6$ protoplasts/ml. The DNA used for transformation is dissolved in Tris-EDTA (TE) buffer solution. 20 µg plasmid DNA is added to each ml protoplast suspension. A plasmid which provides for resistance to phosphinotricine is used as vector (cf. e.g. EP 0 513 849). After the addition of DNA the protoplast suspension is carefully shaken in order to homogenously distribute the DNA in the solution. Immediately afterwards 5 ml PEG solution is added in drops.

By carefully shaking the tubes the PEG solution is distributed homogenously. Afterwards further 5 ml of PEG solution are added and the homogenous mixing is repeated. The protoplasts remain in the PEG solution for 20 minutes at $\pm 2^\circ \text{C}$. Afterwards the protoplasts are sedimented by centrifuging for 3 minutes (100g; 1000 Upm). The supernatant is abandoned. The protoplasts are washed in 20 ml W5 solution by careful shaking and are again subjected to

centrifugation. Then they are resuspended in 20 ml protoplast culture medium, centrifuged anew and again resuspended in culture medium. The titer is adjusted to $6 - 8 \times 10^5$ protoplasts and the protoplasts are cultivated in 3 ml portions in Petri dishes (\varnothing 60 mm, height 15 mm). The Petri dishes are sealed with parafilm and stored in darkness at $25 \pm 2^\circ \text{C}$.

(c) Protoplast culture

During the first 2 - 3 weeks after the protoplast isolation and transformation the protoplasts are cultivated without adding fresh medium. As soon as the cells regenerated from the protoplasts have developed into cell aggregates with more than 20 to 50 cells, 1 ml of fresh protoplast culture medium, containing sucrose as an osmotic (90 g/l), is added.

(d) Selection of transformed maize cells and plant regeneration

3 - 10 days after adding fresh medium the cell aggregates developed from the protoplasts may be plated on Agar media with 100 mg/l L-phosphinothricine. N6-medium with the vitamins of the protoplast culture medium, 90 g/l sucrose and 1.0 mg/l 2.4D is as suitable as an analogous medium such as a medium with the macro- and micro-nutritive salts of the MS medium (Murashige and Skoog (1962), see above).

The calli developed from stably transformed protoplasts may grow further on the selective medium. After 3 to 5 weeks, preferably 4 weeks the transgenic calli may be transferred to fresh selection medium

which also contains 100 mg/l L-phosphinothricine which, however, does no longer contain auxine. Within 3 to 5 weeks approximately 50% of the transgenic maize calli which had integrated the L-phosphinothricine-acetyl-transferase gene into their genome, start to differentiate into plants on this medium in the presence of L-phosphinothricine.

(e) Growing of transgenic regenerative plants

The embryogenical transformed maize tissue is cultivated on hormone-free N6-medium (Chu C.C. et al., Sci. Sin. 16 (1975), 659) in the presence of 5×10^{-4} M L-phosphinothricine. On this medium maize embryos, which express the phosphinothricine-acetyl-transferase gene (PAT gene) in a sufficiently strong manner, develop into plants. Non-transformed embryos or such with only a very weak PAT activity die down. As soon as the leaves of the in-vitro plants have reached a length of 4 to 6 mm, they may be transferred into soil. After washing off the Agar residues at the roots the plants are planted into a mixture of clay, sand, vermiculite and potting soil with the ratio 3:1:1:1 and adapted to the soil culture at 90 - 100% of relative atmospheric humidity during the first 3 days after planting. The growing is carried out in a climate chamber with a 14 hour light period of approximately 25000 lux at the height of the plant at a day/night temperature of $23 \pm 1/17 \pm 1^\circ$ C. The adapted plants are cultivated at an $65 \pm 5\%$ atmospheric humidity.

6. Radioactive marking of DNA fragments

The radioactive marking of DNA fragments was carried out by means of a DNA-Random Primer Labeling Kits by Boehringer (Germany) according to the manufacturer's instructions.

7. Northern Blot Analysis

RNA was isolated from leave tissue according to standard protocols. 50 µg of the RNA was separated on an agarose gel (1.5% agarose, 1 x MEN buffer, 16.6% formaldehyde). After the gel run the gel was briefly washed in water. The RNA was transferred to a Hybond N type nylon membrane (Amersham, UK) with 20 x SSC by means of capillary blot. The membrane was subsequently baked in vacuum for two hours at 80°C.

The membrane was prehybridized in NSEB buffer for two hours at 68°C and subsequently hybridized overnight in NSEB buffer in the presence of the radioactively marked probe at 68°C.

8. Plant maintenance

Potato plants were kept in the greenhouse under the following conditions:

light period	16 hours at 25000 lux and 22°C
dark period	8 hours at 15°C
atmospheric humidity	60%

9. Determination of the amylose/amylopectin ratio in starch obtained from potato plants

Starch was isolated from potato plants according to standard methods and the amylose/amylopectin ratio was determined according to the method described by Hovenkamp-Hermelink et al. (Potato Research 31 (1988) 241-246).

10. Determination of glucose, fructose and sucrose

In order to determine the glucose, fructose and/or sucrose content, small pieces of potato tubers (with a diameter of approx. 10 mm) are frozen in liquid nitrogen and subsequently extracted for 30 min at 80°C in 0.5 ml 10mM HEPES, pH 7.5; 80% (vol./vol.) ethanol. The supernatant containing the soluble components is withdrawn and the volume is determined. The supernatant is used for determining the amount of soluble sugars. The quantitative determination of soluble glucose, fructose and sucrose is carried out in a reaction mixture with the following composition:

100.0 mM imidazole/HCl, pH 6.9

1.5 mM $MgCl_2$

0.5 mM $NADP^+$

1.3 mM ATP

10-50 μ l sample

1.0 U glucose-6-phosphate dehydrogenase from yeast

The reaction mixture is incubated at room temperature for 5 minutes. The subsequent determination of sugars is carried out by means of standard photometric methods by measuring the absorption at 340 nm after successive adding of

1.0 unit of hexokinase from yeast

(for determining glucose)

1.0 unit of phosphoglucosomerase from yeast
(for determining fructose)
and
1.0 unit of invertase from yeast
(for determining sucrose).

Example 1

The isolation of starch granule-bound proteins from potato starch

The isolation of starch granule-bound proteins from potato starch is carried out by means of electroelution in an elution appliance which was constructed analogous to the "Model 442 Electro Eluter" (BIORAD Laboratories Inc., USA) but had a considerably greater volume (approx. 200 ml). 25 g dried starch were dissolved in elution buffer (final volume 80 ml). The starch was derived from potatoes which produce an almost amylose-free starch due to the antisense-expression of a DNA sequence encoding the starch granule-bound starch synthases I (GBSS I) from potato. The suspension was heated to 70-80°C in a water bath. Subsequently 72.07 g urea was added (end concentration 8 M) and the volume was filled up to 180 ml with elution buffer. The starch dissolved during permanent stirring and acquired a paste-like consistency. The proteins were electroeluted from the solution overnight by means of the elution appliance (100 V; 50-60 mA). The eluted proteins were carefully removed from the appliance. Suspended particles were removed in a brief centrifugation. The supernatant was dialyzed at 4°C 2 to 3 times for one hour against dialysis buffer. Subsequently, the volume of the protein solution was determined. The proteins were precipitated by adding ammonium sulfate (final concentration 90 %), which was done during

permanent stirring at 0°C. The precipitated proteins were pelleted by centrifugation and resuspended in protein buffer.

Example 2

Identification and isolation of cDNA sequences encoding starch granule-bound proteins

The proteins isolated according to Example 1 were used for the production of polyclonal antibodies from rabbit, which specifically recognize starch granule-bound proteins.

By means of such antibodies a cDNA expression library was subsequently screened for sequences encoding starch granule-bound proteins, using standard methods.

The expression library was produced as follows:

Poly (A⁺)-mRNA was isolated from potato tubers of the "Berolina" variety. Starting from the poly (A⁺)-mRNA, cDNA was produced according to the Gubler and Hoffmann method (Gene 25 (1983), 263-269), using an Xho I-Oligo d(t)18 primer. This cDNA was cut with Xho I after EcoR I-linker addition and ligated in an oriented manner in a lambda ZAP II vector (Stratagene) cut with EcoR I and Xho I. Approximately 500,000 plaques of a cDNA library constructed in such a way were screened for sequences which were recognized by polyclonal antibodies directed against starch granule-bound proteins.

In order to analyze the phage plaques these were transferred to nitrocellulose filters which had previously been incubated in a 10 mM IPTG solution for 30 to 60 minutes and had subsequently been dried on filter paper. The transfer took place at 37°C for 3 hours. Subsequently, the filters are incubated at room temperature for 30 minutes in block reagent and washed for 5-10 minutes in TBST buffer. The filters were shaken with the polyclonal antibodies directed against starch granule-bound proteins in a suitable dilution for one hour at room

temperature or for 16 hours at 4°C. The identification of plaques expressing a protein which was recognized by the polyclonal antibodies was carried out by means of the "Blotting detection kit for rabbit antibodies RPN 23" (Amersham UK) according to the manufacturer's instructions.

Phage clones of the cDNA library expressing a protein which was recognized by the polyclonal antibodies were further purified by using standard methods.

By means of the in-vivo excision method, E.coli clones were obtained from positive phage clones containing a double-stranded pBluescript plasmid with the corresponding cDNA insertion. After checking the size and the restriction pattern of the insertions a suitable clone, pRL1, was further analyzed.

Example 3

Sequence analysis of the cDNA insertion of the plasmid pRL1

From an E.coli clone obtained according to Example 2 the plasmid pRL1 was isolated and a part of the sequence of its cDNA insertion was determined by standard procedures using the dideoxynucleotide method (Sanger et al., Proc. Natl. Acad. Sci. USA 74 (1977), 5463-5467). The insertion has a length of about 2450 bp. A part of the nucleotide sequence as well as the amino acid sequence derived therefrom is indicated under Seq ID No. 3 and under Seq ID No. 4.

A sequence analysis and a sequence comparison with known DNA sequences showed that the sequence indicated under Seq ID No. 3 is new and exhibits no significant homology to DNA sequences known so far. Moreover, the sequence analysis showed that the cDNA insertion is only a partial cDNA in which a part of the coding region at the 5'-end is missing.

Example 4

Identification and isolation of a complete cDNA encoding a
starch granule-bound protein from Solanum tuberosum

In order to isolate a complete cDNA corresponding to the partial cDNA insertion of the plasmid pRL1, a further cDNA library was produced. This was a guard-cell-specific cDNA library from *Solanum tuberosum* which was constructed as follows:

At first epidermis fragments from leaves of "Desirée" variety potato plants were produced essentially according to the Hedrich et al. method (Plant Physiol. 89 (1989), 148), by harvesting approximately 60 leaves of six-weeks-old potato plants kept in the greenhouse. The center nerve was removed from the leaves. The leaves were subsequently crushed in a big "Waring blender" (with a volume of 1 liter) four times in cooled, distilled H₂O on the highest level for 15 seconds each. The suspension was filtered through a nylon sieve with a mesh size of 220 µm (Nybolt, Zurich, Switzerland) and washed in cold distilled water several times. The suspension itself was filtered through a 220 µm nylon sieve and intensely washed with cold distilled water. The residues (epidermis fragments) were crushed in a smaller "Waring blender" (with a volume of 250 ml) four times in distilled water and ice on a lower level for 15 seconds each. The suspension was filtered through a 220 µm nylon sieve and washed intensely with cold distilled water. The epidermis fragments (residues) were microscopically examined for contamination by mesophyll cells. If contamination occurred the crushing step was repeated in a small "Waring blender". The disruption of the guard cells of the epidermis fragments was carried out by means of pulverizing in liquid nitrogen in a cooled mortar for approximately two hours. In order to examine

the disruption of the guard cells, probes were regularly taken and microscopically examined. After two hours, or if a sufficiently high amount of guard cells had been disrupted, the obtained powder was filled into a reaction tube (with a volume of 50 ml) and resuspended in one volume GTC buffer (Chirgwin et al., Biochem. 18. (1979), 5294-5299). The suspension was centrifuged and the supernatant was filtered through Miracloth (Calbiochem, La Jolla, California). The filtrate was subjected to ultracentrifugation for 16 hours, as described in Glisin et al. (Biochemistry 13 (1974), 2633-2637) and Mornex et al. (J. Clin. Inves. 77 (1986), 1952-1961). After the centrifugation the RNA precipitate was dissolved in 250 μ l GTC buffer. The RNA was precipitated by adding 0.05 volumes of 1 M acetic acid and 0.7 volumes of ethanol. The RNA was precipitated by centrifugation and the precipitate was washed with 3 M sodium acetate (pH 4.8) and 70% ethanol. The RNA was briefly dried and dissolved in DEPC treated water.

Poly A⁺-RNA was isolated from the isolated RNA according to standard methods. Starting from the poly(A⁺)-mRNA, cDNA was produced according to the Gubler and Hoffmann method (Gene 25 (1983), 263-269) by means of a Xho I-oligo d(t)₁₈ primer. This cDNA was cut with Xho I after EcoR I-linker addition and ligated in an oriented manner in a lambda ZAP II vector (Stratagene GmbH, Heidelberg, Germany) cut with EcoR I and Xho I. The packaging in phage heads was carried out using the Gigapack II Gold kit (Stratagene GmbH, Heidelberg, Germany) according to the manufacturer's instructions.

From such a cDNA library phage clones hybridizing with the cDNA insertion of the pRL1 plasmid were isolated and purified according to standard methods. By means of the in vivo excision method E.coli clones were obtained from positive phage clones containing a double-stranded pBluescript plasmid with the corresponding cDNA insertion. After checking the size and the restriction pattern of the insertions, suitable clones were

subjected to restriction mapping and sequence analysis. From a suitable clone the plasmid pRL2 (DSM 10225) was isolated which contains a complete cDNA which encodes a starch granule-bound protein from potato.

Example 5

Sequence analysis of the cDNA insertion of the pRL2 plasmid

The nucleotide sequence of the cDNA insertion of the pRL2 plasmid was determined as described in Example 3. The insertion has a length of 4856 bp. The nucleotide sequence as well as the amino acid sequence derived therefrom is indicated in Seq ID No. 1 and/or Seq ID No. 2. In the following, the corresponding gene will be called RL-gene. The protein encoded by the coding region will be called R1 enzyme.

Example 6

The construction of the plasmid p35S-anti-RL and the introduction of the plasmid into the genome of potato plants

By means of the restriction endonuclease Asp718 a DNA fragment with an approximate length of 1800 bp was isolated from the pRL1 plasmid. This corresponds to the DNA sequence indicated under Seq ID No. 3 and contains a part of the open reading frame. The fragment was ligated into the binary vector pBinAR cut with Asp718 (Höfgen and Willmitzer, Plant Sci. 66 (1990), 221-230). This is a derivative of the binary vector pBin19 (Bevan, Nucl. Acids Res. 12 (1984), 8711-8721). pBinAR was constructed as follows:

A fragment with a length of 529 bp comprising the nucleotides 6909-7437 of the 35S promoter of the cauliflower-mosaic virus

(Franck et al., Cell 21 (1980), 285-294) was isolated from the plasmid pDH51 (Pietrzak et al., Nucl. Acids Res. 14, 5857-5868) as an EcoR I/Kpn I fragment and ligated between the EcoR I and the Kpn I sites of the pBin19 polylinker. This led to the plasmid pBin19-A.

By means of the restriction endonucleases Pvu II and Hind III a fragment with a length of 192 bp was isolated from the plasmid pAGV40 (Herrera-Estrella et al., Nature 303, 209-213) comprising the polyadenylation signal of gene 3 of the T-DNA of the Ti-plasmid pTiACH5 (Gielen et al., EMBO J. 3, 835-846) (nucleotides 11749-11939). After the addition of Sph I-linkers to the Pvu I site the fragment was ligated between the Sph I and Hind III sites of pBin19-A. This led to plasmid pBinAR.

By means of restriction and sequence analysis recombinant vectors were identified in which the DNA fragment is inserted in the vector in such a way that a part of the coding region of the cDNA insertion from pRL1 is linked with the 35S promoter in antisense orientation. The resulting plasmid p35S-anti-RL is shown in Figure 1.

By inserting the cDNA fragment an expression cassette is produced which consists of the fragments A, B and C:

Fragment A (529 bp) contains the 35S promoter of the cauliflower-mosaic virus (CaMV). The fragment comprises the nucleotides 6909 to 7437 of the CaMV (Franck et al., Cell 21 (1980), 285-294).

Apart from flanking regions, fragment B contains a part of the protein encoding cDNA insertion from plasmid pRL1. This was isolated as an Asp718 fragment of pRL1 as described above and fused to the 35S promoter in antisense orientation.

Fragment C (192 bp) contains the polyadenylation signal of gene 3 of the T-DNA of the Ti-plasmid pTiACH5 (Gielen et al., EMBO J. 3 (1984), 835-846).

The plasmid p35S-anti-RL has a size of approximately 12.8 kb.

The plasmid was transferred into potato plants by means of Agrobacteria-mediated transformation, as described above. From the transformed cells whole plants were regenerated. The transformed plants were cultivated under greenhouse conditions. By analyzing total RNA in a Northern Blot analysis concerning the disappearance of the transcripts complementary to the cDNA, the success of the genetic modification of the plants was assessed. For this purpose, total RNA was isolated from leaves of transformed plants according to standard methods and subsequently separated electrophoretically on an agarose gel. Then it was transferred onto a nylon membrane and hybridized with a radioactively labelled probe having the sequence indicated under Seq ID No. 1 or a part thereof. In about 5-10% of the transformed plants the band indicating the specific transcript under Seq ID No. 1 was missing in the Northern Blot Analysis. The plants were used for analyzing the starch quality.

Example 7

The construction of the plasmid pB33-anti-RL and the introduction of the plasmid into the genome of potato plants

By means of the restriction endonuclease Asp718, a DNA fragment with an approximate length of 1800 bp, which comprises a part of the open reading frame of the cDNA insertion was isolated from the plasmid pRL1 and was ligated into the vector B33-Hyg which was cut with Asp718. This vector was constructed as follows:

The 35S promoter was removed from the pBinAR Hyg vector (DSM 9505) by means of the restriction endonucleases EcoR I and Asp718. A fragment with a length of about 1526 bp comprising the B33 promoter was isolated from the plasmid p33-anti-BE (DSM

6146) by means of EcoR I and Asp718 and inserted into the pBinAR Hyg vector (DSM 9505) cut with EcoR I and Asp718.

By inserting the cDNA fragment into the Asp718 site of the B33-Hyg plasmid, an expression cassette is produced which consists of the fragments A, B and C as follows (Figure 4):

Fragment A contains the B33 promoter from *Solanum tuberosum* (EP 3775 092; Rocha-Sosa et al., EMBO J. 8 (1989), 23-29).

Apart from flanking regions, fragment B contains a part of the protein encoding region of the cDNA insertion from the pRL1 plasmid. This was isolated as an Asp718 fragment from pRL1 as described above and fused to the 35S promoter in antisense orientation.

Fragment C (192 bp) contains the polyadenylation signal of gene 3 of the T-DNA of the Ti-plasmid pTiACH5 (Gielen et al., EMBO J. 3 (1984), 835-846).

The plasmid pB33-anti-RL has a size of approximately 12.8 kb.

The plasmid was transferred into potato plants by means of *Agrobacteria*-mediated transformation, as described above. From the transformed cells whole plants were regenerated. The transformed plants were cultivated under greenhouse conditions. By analyzing total RNA in a Northern Blot analysis concerning the disappearance of the transcripts complementary to the cDNA the success of the genetic modification of the plants was assessed. For this purpose, total RNA was isolated from leaves of transformed plants according to standard methods and subsequently separated electrophoretically on an agarose gel. Then it was transferred onto a nylon membrane and hybridized with a radioactively labelled probe showing the sequence indicated under Seq ID No. 1 or a part thereof. In about 5-10% of the transformed plants the band indicating the transcript hybridizing with the cDNA of the invention was missing in the Northern Blot Analysis. From these plants starch was isolated from tubers and analyzed as described in Example 8.

Example 8

Analysis of the transformed potato plants

The potato plants transformed according to Example 6 and Example 7 were examined with regard to the properties of the synthesized starch. Analyses were carried out with various lines of the potato plants which had been transformed with the plasmid p35S-anti-RL or the plasmid pB33-anti-RL and which in Northern Blot analysis had not exhibited the band indicating transcripts hybridizing to the DNA sequences of the invention.

a) Determination of the viscosity of watery solutions of the starch

In order to determine the viscosity of the watery solutions of the starch synthesized in transformed potato plants, starch was isolated from tubers of plants which had been transformed with the plasmid p35S-anti-RL or the plasmid pB33-anti-RL using standard methods. 30 g of starch were each taken up in 450 ml H₂O and used for analysis in an E viscograph (Brabender OHG Duisburg (Germany)). The appliance was used according to the manufacturer's instructions. In order to determine the viscosity of the watery solution of the starch, the starch suspension was first heated from 50°C to 96°C at a speed of 3°C per minute. The temperature was subsequently kept at 96°C for 30 min. The solution was then cooled from 96°C to 50°C at a speed of 3°C per minute. During the whole process the viscosity was determined. Representative results of such measurements are set forth in the form of graphs in Figures 3, 4 and 5, in which the viscosity is

shown depending on time. Figure 3 shows a typical Brabender graph for starch isolated from wildtype-plants of the potatoe variety Désirée. Figures 4 and 5 show a typical Brabender graph for starch isolated from potato plants which had been transformed with the plasmid p35S-anti-RL or pB33-anti-RL. From these graphs characteristic values may be deduced.

The characteristic values for wildtype-plants are as follows:

Table 1

Value	Time [min : sec]	Torque [BE]	Temperature [°C]
A	6 : 30	60.5 ± 17.7	69.9 ± 0.57
B	11 : 30	1838.0 ± 161.2	86.0 ± 2.1
C	15 : 15	1412.0 ± 18.4	96.0
D	45 : 15	526.0 ± 17.0	96.0
E	60 : 30	812.0 ± 8.5	50.0
F	70 : 45	853.0 ± 5.7	50.0

The values represent the average values obtained from two different measurements.

In Table 1 and the following Tables 2 and 3 the abbreviations signify the following:

- A: start of pastification
- B: maximum viscosity
- C: start of 96°C-period
- D: start of cooling-off time
- E: end of cooling-off time
- F: end of the end-50°C period

For plants which had been transformed with the plasmid p35S-anti-RL (line P2), the characteristic values are the following:

Table 2

Value	Time [min : sec]	Torque [BE]	Temperature [°C]
A	6 : 00	50.0	69.0
B	14 : 00	820.0	93.0
C	15 : 15	815.0	96.0
D	45 : 15	680.0	96.0
E	60 : 30	1150.0	50.0
F	70 : 45	1200.0	50.0

For plants which had been transformed with the plasmid pB33-anti-RL (line P3), the characteristic values are the following:

Table 3

Value	Time [min : sec]	Torque [BE]	Temperature [°C]
A	7:0	31.0	71.0
B	12:45	671.0	88.3
C	15:15	662.0	96.0
D	45:15	607.0	96.0
E	60:30	1063.0	50.0
F	70:45	1021.0	50.0

Figures 3, 4 and 5 explicitly show that the starch obtained from transformed plants differs from starch from wildtype plants particularly in that the viscosity increases only very slightly during heating. Thus, during heating the maximum viscosity of the modified starch from transformed plants is more than 50% lower than in the case of wildtype starch.

During cooling, on the other hand, the viscosity of the starch isolated from transformed plants increases more than in the case of wildtype-plants.

b) Determination of the phosphate content of the starch

The phosphate content of the starch was determined by measuring the amount of phosphate bound to the C-6-position of the glucose residues. For this purpose, starch was first degraded by acid hydrolysis and the glucose-6-phosphate content was subsequently determined by means of an enzyme test, as described in the following.

100 mg starch were incubated in 500 μ l 0.7 N HCl for 4 hours at 100°C. After acid hydrolysis 10 μ l of the reaction were added to 600 μ l imidazole buffer (100 mM imidazole, 5 mM MgCl₂, pH 6.9, 0.4 mM NAD⁺). The amount of glucose-6-phosphate in the reaction mixture was determined by conversion with the enzyme glucose-6-phosphate-dehydrogenase. For this purpose, 1 U glucose-6-phosphate-dehydrogenase (from *Leuconostoc mesenteroides* (Boehringer Mannheim)) was added to the reaction mixture and the amount of produced NADH was determined by measuring the absorption at 340 nm.

The glucose-6-phosphate content of 1 mg starch is indicated in the following table for non-transformed potato plants of the variety Désirée as well as for two lines (P1 (35S-anti-RL); P2(35S-anti-RL)) of transgenic potato plants which had been transformed with the plasmid p35S-anti-RL.

Table 4

Plants	nmol glucose-6-phosphate/mg starch	%
Wildtype	12.89 \pm 1.34	100
P1 (35S-anti-RL)	2.25 \pm 0.41	17.4
P2 (35S-anti-RL)	1.25 \pm 0	9.7

The following table shows the glucose-6-phosphate content per milligram starch in potato plants which were transformed with the plasmid pB33-anti-RL, compared to starch from non-transformed plants (*S. tuberosum* c.v. Désirée).

Table 5

Plants	nmol glucose-6-phosphate/mg starch	%
Wildtype	9.80 \pm 0.68	100
7	4.50 \pm 0.73	45.9
37	2.64 \pm 0.99	26.9
45	1.14 \pm 0.44	11.6
31	1.25 \pm 0.49	12.8

The plants 7, 37, 45 and 31 represent independent transformants which had been transformed with the plasmid pB33-anti-RL. Plant 37 represents line P3 for which a Brabender graph is plotted in Figure 5.

The values show that the phosphate content of the modified starch from transgenic potato plants is at least 50% lower when compared to starch from wildtype plants.

- c) Determination of glucose, fructose and sucrose content of tubers after storage at 4°C

Tubers of plants from various transgenic lines which had been transformed with the antisense-construct p35S-anti-RL

as well as tubers of wildtype plants were stored at 4°C or, respectively, at 20°C in darkness, for two months. Subsequently, the amounts of glucose, fructose and sucrose were determined. For two transgenic lines the representative values obtained were the following:

Table 6

	Glucose		Fructose		Sucrose	
	20°C	4°C	20°C	4°C	20°C	4°C
Wildtype	0.84	55.4	0.62	52.8	8.5	13.1
cv Désirée						
Transgenic	1.12	6.7	0.75	7.8	7.5	10.1
line 15						
Transgenic	1.00	6.4	0.75	7.5	6.9	6.9
line 11						

The values in the table are indicated in μmol hexose or sucrose/g fresh weight.

From the values of Table 6 it becomes obvious that the accumulation of reducing sugars in the tubers is considerably lower in transgenic plants stored at 4°C than in wildtype plants.

Altogether the modified starch isolated from transgenic potato plants resembles starch from maize-wildtype plants. However, in comparison it has the advantage that its taste is neutral and that it is therefore more suitable for various uses in the foodstuffs area.

Example 9

Expression of the cDNA insertion of the pRL2 plasmid in E.coli(a) Transformation of bacterial cells

In order to express the cDNA insertion of the plasmid pRL2 the cells of the E.coli strain DH5 α are first transformed with the pACAC plasmid. This plasmid contains a DNA fragment encoding the ADP-glucose-pyrophosphorylase (AGPase) from E.coli, under the control of the lac Z promoter. The fragment had been isolated from the vector pEcA-15 as a DraI/HaeII fragment with a size of about 1.7 kb (see B. Müller-Röber (1992), dissertation, FU Berlin) and after filling in its sticky ends it had been cloned into a pACAC184 vector linearized with HindIII. The expression of AGPase is to cause an increase of the glycogen synthesis in transformed E.coli cells. The cells transformed in such a way will in the following be named E.coli-K1-cells.

In order to determine the enzyme activity of the protein encoded by the cDNA of plasmid pRL2, E.coli-K1-cells were transformed with the pRL2 plasmid. The transformed E.coli cells which contain the pACAC plasmid as well as the pRL2 plasmid will in the following be named E.coli-K2-cells.

The transfer of the plasmid DNA into the bacterial cells was carried out according to the Hanahan method (J. Mol. Biol. 166 (1983), 557-580). The transformed E.coli cells were plated onto agar culture dishes with the following composition:

YT medium containing

1,5% Bacto agar

50 mM sodium phosphate buffer, pH 7.2
1% glucose
10 µg/ml chloramphenicol in the case of E.coli-K1-cells
or
10 µg/ml chloramphenicol and
10 µg/ml ampicillin in the case of E.coli-K2-cells.

Escherichia coli cells of the DH5α strain which had been transformed with the plasmid pRL2 + pACAC (E.coli-K2-cells) and also - for control - solely with the pACAC plasmid (E.coli-K1-cells), were raised on agar plates. The formed glycogen of the various cultures was examined with respect to the degree of phosphorylization (at the C-6 position of the glucose molecule), as described in the following.

(b) Isolation of bacterial glycogen

In order to isolate bacterial glycogen, the bacteria colony which had grown after transformation was floated from each 6 agar plates (Ø 135 mm) with 5 ml YT medium for each plate. The bacterial suspension was centrifuged at 4500 xg for 5 minutes. The bacterial precipitate was resuspended in 10 ml YT medium. Disruption of the bacteria was carried out by adding 2 volumes of disruption medium (0.2 N NaOH; 1% SDS) and by incubation at room temperature for 5 minutes. By adding 3 volumes of EtOH abs., incubating at 4°C for 30 minutes and subsequent centrifuging at 8000 gx for 15 minutes, the glycogen was sedimented. Then the precipitate was washed with 100 ml of 70% EtOH and again sedimented by means of a centrifugation step (10 minutes at 8000 xg). The washing procedure was repeated four times.

(c) Determination of the total glycogen content

The isolated and sedimented glycogen was first degraded into single glucose molecules by means of acidic hydrolysis (dissolving of the precipitate in 2 ml 0.7 N HCl; incubation for 4 hours at 100°C). The glucose content of the solution was determined by means of coupled enzymatic reaction of a starch test with a photometer (Kontron) at a wave length of 340 nm according to the manufacturer's (Boehringer Mannheim) instructions.

The reaction buffer contains:

100	mM MOPS, pH 7.5
10	mM MgCl ₂
2	mM EDTA
0.25	mM NADP
1	mM ATP
1	U/ml glucose-6-phosphate-dehydrogenase
2	U/ml hexokinase

The measurement was carried out at 25°C with 10 µl glucose solution.

(d) Determination of the glucose-6-phosphate content

In order to determine the content of glucose molecules phosphorylated at the C-6 position, equal amounts of glucose of the various bacterial cultures were used. By adding the same volumes of 0.7 N KOH to the glycogens degraded into its glucose molecules by acidic hydrolysis (as above), the solution was neutralized.

The reaction buffer contains:

100 mM MOPS, pH 7.5
10 mM MgCl_2
2 mM EDTA
0.25 mM NADP
2 U/ml glucose-6-phosphate-
dehydrogenase

The measurement was carried out at 25°C with 100 to 150 μl glucose solution.

(e) Identification of an enzyme activity phosphorylating bacterial glycogen

The results of the determination of the phosphate content of the glycogen synthesized in the bacterial cells show that the glycogen of the E.coli cells, which had been transformed with the pACAC + pRL2 plasmids, exhibits a $290 \pm 25\%$ increased phosphorylation at the C-6 position of the glucose when comparing with the control reaction (E.coli cells transformed with the pACYC) (see the following table).

E.coli cells	glucose-6-phosphate: glucose in glycogen
E.coli-K1	1 : (4600 \pm 1150)
E.coli-K2	1 : (1570 \pm 390)

The degrees of phosphorylation indicated herein are the average value of at least 6 measurements starting from 6 independent transformations and glycogen isolations.

Example 10

Integration of the plasmid p35S-anti-RL in combination with the plasmid p35SH-anti-BE into the genome of potato plants

The plasmid p35S-anti-RL was constructed as described in Example 6. The plasmid p35SH-anti-BE was constructed as described in the application WO95/07355, Example 3. Both plasmids were sequentially transferred into potato plants by means of the Agrobacterium mediated transformation as described above. For this purpose, the plasmid p35SH-anti-BE was first transformed in potato plants. Whole plants were regenerated and selected for a reduced expression of the branching enzyme gene. Subsequently, the plasmid p35S-anti-RL was transformed into the transgenic plants already showing a reduced expression of the branching enzyme. From the transformed cells transgenic plants were again regenerated and the transformed plants were cultivated under greenhouse conditions. By analyzing total RNA in an RNA Blot analysis with respect to the disappearance of the transcripts complementary to the branching enzyme cDNA or the RL cDNA, the success of the genetic modification of the plants with respect to a highly reduced expression of the branching enzyme gene as well as with respect to a highly reduced expression of the RL gene was assessed. For this purpose, total RNA was isolated from leaves of transformed plants according to the described methods and subsequently separated by means of gel electrophoresis, transferred onto a membrane, hybridized with a radioactively labelled probe showing the sequence indicated under Seq ID No. 1 or a part thereof and then hybridized with a radioactively labelled probe showing the sequence of the branching enzyme cDNA (cf. WO92/14827, Example 1) or a part thereof. In about 5-10% of the transformed plants the band indicating the specific transcript of the sequence indicated under Seq ID No. 1 as well as the

band indicating the specific transcript of the branching enzyme cDNA (cf. WO92/14827) was missing in the RNA Blot Analysis. These plants, which were designated R4 plants were used for analyzing the quality of the starch contained in tubers.

Example 11

Integration of the plasmid pB33-anti-RL in combination with the plasmid pB33-anti-GBSSI into the genome of potato plants

The plasmid pB33-anti-RL was constructed as described in Example 7. The plasmid pB33-anti-GBSSI was constructed as follows:

The DraI/DraI fragment of the promoter region of the patatin class I gene B33 from *Solanum tuberosum* comprising the nucleotides -1512 to +14 (Rocha-Sosa et al., EMBO J 8 (1989), 23-29) was ligated into the SmaI site of the pUC19 plasmid. From the resulting plasmid the promoter fragment was ligated into the polylinker region of the pBin19 plasmid (Bevan, Nucleic Acids Research 12 (1984), 8711-8721) as an EcoRI/HindIII fragment. Subsequently, the 3' EcoRI fragment 1181 to 2511 of the GBSSI gene of *Solanum tuberosum* (Hegersberg, dissertation (1988), University of Cologne) was ligated into the EcoRI site of the resulting plasmid.

Both plasmids were transferred sequentially into potato plants by means of *Agrobacterium* mediated transformation as described in Example 10. From the transformed cells plants were regenerated and the transformed plants were cultivated under greenhouse conditions. By analyzing the complete RNA in a RNA Blot analysis with regard to the disappearance of the transcripts complementary to the two cDNAs, the success of the genetic modification of the plants was assessed. For this

purpose, total RNA was isolated from tubers of transformed plants according to standard methods and subsequently separated on agarose gel by means of gel electrophoresis, transferred onto a membrane and hybridized with a radioactively labelled probe showing the sequence indicated under Seq ID No. 1 or a part thereof. Afterwards, the same membrane was hybridized with a radioactively labelled probe having the sequence of the GBSSI gene or a part of this sequence (Hegersberg, dissertation (1988) University of Cologne). In about 5-10% of the transformed plants the band indicating the transcripts hybridizing to the cDNA of the invention or the GBSSI cDNA were missing in the RNA Blot Analysis. From the tubers of these plants, which were designated R3 plants, starch was isolated and analyzed.

Example 12

Starch analysis of R4 plants

The potato plants transformed according to Example 10 were examined with respect to the properties of the synthesized starch. The analyses were carried out with various lines of the potato plants which had been transformed with the plasmids p35S-anti-RL and p35SH-anti-BE and which did no longer - or only in extremely reduced form - show the bands indicating transcripts hybridizing to the DNA sequences of the invention or to the sequences of the branching cDNA in RNA Blot analysis.

- a) Determination of the viscosity of watery solutions of the starch

In order to determine the viscosity of the watery solutions of the starch synthesized in transformed potato

plants, starch was isolated from tubers of plants which had been transformed with the plasmid p35S-anti-RL and the plasmid p35SH-anti-BE. 2 g of starch were each dissolved in 25 ml H₂O and used for analysis with a Rapid Visco Analyser (Newport Scientific Pty Ltd, Investment Support Group, Warriewood NSW 2102, Australia). The equipment was used according to the instructions of the manufacturer. In order to determine the viscosity of the watery solution of the starch, the starch suspension was first heated from 50°C to 95°C with a speed of 12°C per minute. The temperature was then kept at 95°C for 2.5 minutes. Afterwards, the solution was cooled from 95°C to 50°C with a speed of 12°C per minute. During the whole process the viscosity was measured. Representative results of such measurements are set forth in the form of graphs in which the viscosity is shown depending on time. Figure 6 shows a typical RVA graph for starch isolated from the wildtype-plants of potato of the variety Désirée. Lines 2 and 3 show a typical RVA graph for starch isolated from the tubers of plants which had been transformed with the plasmid p35SH-anti-BE and with the plasmid p35S-anti-RL, respectively. Line 4 shows a typical RVA graph for starch isolated from tubers of plants which had been transformed with plasmid p35SH-anti-BE in combination with plasmid p35S-anti-RL. Line 4 is characterized in that there is no temperature-dependent increase of viscosity.

b) Determination of the amylose/amylopectin ratio

Starch which was isolated from the tubers of transformed potato plants was examined with respect to the ratio of amylose to amylopectin. The plant line R4-1 (shown in line 4 of Fig. 6) exhibited an amylose content of more than

70%. For the plant line R4-3 an amylose value of 27% was measured, whereas the amylose content in wildtype starch of the Désirée variety rates between 19 and 22%.

Example 13

Starch analysis of R3 plants

The potato plants transformed according to Example 11 were examined with respect to the properties of the synthesized starch. The analyses were carried out with various lines of the potato plants which had been transformed with the plasmids pB33-anti-RL and pB33-anti-GBSSI and which did no longer - or only in extremely reduced form - show the bands indicating transcripts hybridizing to the DNA sequences of the invention or to the sequences of the GBSSI cDNA in RNA Blot analysis.

a) Determination of the viscosity of watery solutions of the starch

In order to determine the viscosity of the watery solution of the starch synthesized in transformed potato plants, starch was isolated from tubers of plants which had been transformed with the plasmid pB33-anti-RL in combination with the plasmid pB33-anti-GBSSI. The viscosity was determined by means of a Rapid Visco Analyser according to the method described in Example 12, part a. The results are indicated in Figure 7. In line 1, Figure 7 shows a typical RVA graph for starch isolated from the wildtype-plants of the Désirée potato variety. Lines 2 and 3 show typical RVA graphs for starches isolated from potato plants which had been transformed with the plasmid pB33-anti-GBSSI and with the plasmid p35S-anti-RL,

respectively. Line 4 shows a typical RVA graph for starch isolated from potato plants which had been transformed with the plasmid pB33-anti-GBSSI in combination with the plasmid pB33-anti-RL. This graph is characterized in that the maximum viscosity and the increase of viscosity at 50°C are missing. Furthermore, this starch is characterized in that the glue obtained after RVA treatment exhibits almost no retrogradation after incubating at room temperature for several days.

b) Determination of the amylose/amylopectin ratio

Starch which was isolated from the tubers of transformed potato plants was examined with respect to the ratio of amylose to amylopectin. The plant line R3-5 (shown in line 4 of Fig. 7) exhibited an amylose content of less than 4%. For the plant line R3-6 an amylose content of less than 3% was measured. The amylose content in wildtype starch of the Désirée variety rates between 19 and 22%.

c) Determination of the phosphate content of starch

The phosphate content of the starch was determined by measuring the amount of phosphate bound to the C-6-position of the glucose residues. For this purpose, starch was first degraded by acid hydrolysis and the glucose-6-phosphate content was subsequently determined by means of an enzyme test, as described in the following.

100 mg starch were incubated in 500 µl 0.7 N HCl for 4 hours at 100°C. After acid hydrolysis 10 µl of the reaction mixture were added to 600 µl imidazole buffer (100 mM imidazole, 5 mM MgCl₂, pH 6.9, 0.4 mM NAD⁺). The amount of glucose-6-phosphate in the preparation is

determined by conversion with the enzyme glucose-6-phosphate-dehydrogenase. For this purpose, 1 U glucose-6-phosphate-dehydrogenase (from *Leuconostoc mesenteroides* (Boehringer Mannheim)) was added to the reaction mixture and the amount of produced NADH was determined by measuring the absorption at 340 nm.

The glucose-6-phosphate content of 1 mg starch is indicated in the following table for non-transformed potato plants of the variety Désirée as well as for the R3-5 and the R3-6 line of transgenic potato plants which had been transformed with the plasmid pB33-anti-RL in combination with the plasmid pB33-anti-GBSSI. As a comparison, the value of the starch from the so-called waxy potato (US2-10) which had been transformed with the plasmid pB33-anti-GBSSI, is also indicated.

Table 7

Plants	nmol glucose-6-phosphate/mg starch	%
Wildtype	9.80 ± 0.68	100
R3-5	1.32 ± 0.10	13
R3-6	1.37 ± 0.15	14
US2-10	10.82 ± 0.42	110

Example 14

Isolation of a cDNA sequence encoding an R1 enzyme from Zea
mays

Bacteria of the XL1-Blue strain were infected with lambda phages, the phage heads of which contained a cDNA library of endosperm tissue from Zea mays (Stratagene, Heidelberg). The infected E.coli cells were plated on a medium in Petri dishes

with a density of about 25000 plaques per approx. 75 cm². After about 9 hours of incubation nitro cellulose filters were laid on the lysed bacteria and were removed after one minute. The filter was first incubated in 0.5 M NaOH, 1.5 M NaCl for two minutes, then in 0.5 M Tris HCl pH 7.0 for two minutes and subsequently washed in 2x SSC for two minutes. After drying and fixing by UV crosslinking the filters were incubated in buffer A for 3 hours before a radioactively labelled DNA probe (random priming) was added. A fragment of the pRL2 plasmid DNA insertion (see Examples 4 and 5) with a size of approximately 2.7 was used as a probe. This fragment was cut with the restriction enzymes XhoI and HindIII and represented the 3' end of the cDNA insertion in pRL2 (see Figure 8).

After hybridizing for 12 hours at 48°C the filters were washed for 1 x 10 minutes in 2x SSC/1 % SDS at room temperature and then 2 x 20 minutes in 1 x SSC/0.5 % SDS at 35°C and subsequently autoradiographed.

Phage clones comprising a cDNA insertion were singled out in three screening cycles. Thereby, when screening about 1,500,000 phage plaques approximately 6 plaques were identified.

These positive phage clones were used for the in vivo excision of a pBluescript plasmid according to standard methods. The DNA sequences of the corresponding insertions were determined according to the method of Sanger et al. (Proc. Natl. Acad. Sci. USA 74 (1977), 5463-5467). Thus, a number of clones could be identified containing insertions encoding an R1 enzyme from maize. The cDNA insertion of a suitable clone, R1M, was completely determined. The nucleic acid sequence is indicated in Seq ID No. 5. The amino acid sequence derived therefrom is indicated in Seq ID No. 6.

A suitable cDNA insertion of the R1M clone was isolated from the pBluescript derivative by NotI and XhoI by means of standard methods (Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd edition, Cold Spring Harbour Laboratory

Press, (1989), NY, USA). The sticky ends were filled in and the fragment was inserted into the pUBIbar vector at the HpaI site. This plasmid may be used for transforming plant cells, particularly maize, according to the methods described above. Since the sequence depicted in Seq ID No. 5 represents only a partial cDNA sequence, further techniques were applied to isolate sequences representing the 5' end of the cDNA. For this purpose polyA⁺ RNA was isolated from leaf tissue of maize according to standard methods. The isolated RNA was used for a polymerase chain reaction using the TitanTM One Tube RT-PCR system (Boehringer Mannheim, Germany) according to the instructions of the manufacturer. In this reaction the RNA is transcribed in a first step into cDNA which is then used as a template for the PCR. As primers the following oligonucleotides were used:

Primer 1 (Seq ID No. 9):

5' GCAAAGTTTT CAAGGACAAG ACTGATGAAG 3'

Primer 2 (Seq ID No. 10):

5' CCAGATGGCA CGACAGTGTA CAAGAACA 3'

and

Primer 6 (Seq ID No. 11):

5' AATGACTGCA AAGGIGGIAT GATGGA 3'

The combination of primers 1 and 6 led to a 560 bp fragment. The primer combination 1 and 2 led to a PCR fragment of 2289 bp. Both fragments were sequenced. The obtained sequence represents most of the 5' end of the cDNA. The complete sequence of the partial cDNA clone and the sequences obtained by PCR as described above is depicted in Seq ID No. 7. The derived amino acid sequence is depicted in Seq ID No. 8. Comparison with the full-length cDNA of potato revealed that the obtained sequence is probably not yet complete and that about 420 bp of the 5' end are missing. This missing sequence

can be completed by methods well known to the person skilled in the art. It is, for example, possible to isolate the 5' end of the cDNA using the 5'-RACE method (rapid amplification of cDNA ends). With this method an unknown 5'-end of a cDNA can be amplified by PCR. This method is normally used to produce cDNA which, in comparison to a known cDNA, is extended at the 5'-end. In order to apply the 5'-RACE method one can use, e.g., the Marathon-cDNA amplification kit (Clontech).

Other possibilities to isolate the complete cDNA are further PCRs using, for example, a lambda ZAP cDNA library of maize (Stratagene), immuno screening of expression libraries or the use of standard hybridization methods.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: PlantTec Biotechnologie GmbH Forschung&Entwicklung
- (B) STREET ADDRESS: Hermannswerder 14
- (C) CITY: Potsdam
- (E) COUNTRY: DE
- (F) POSTAL CODE: 14473

(ii) TITLE OF INVENTION: Novel nucleic acid molecules from maize and their use for the production of modified starch

(iii) NUMBER OF SEQUENCES: 11

(iv) COMPUTER-READABLE VERSION:

- (A) DATA CARRIER: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPA)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4856 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Solanum tuberosum
- (B) STRAIN: C.V. Berolina

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 105...4497

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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                                     Met Ser Asn Ser
                                     1

TTA GGG AAT AAC TTG CTG TAC CAG GGA TTC CTA ACC TCA ACA GTG TTG      164
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  5              10              15              20

GAA CAT AAA AGT AGA ATC AGT CCT CCT TGT GTT GGA GGC AAT TCT TTG      212
Glu His Lys Ser Arg Ile Ser Pro Pro Cys Val Gly Gly Asn Ser Leu
      25              30              35

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Arg Ala Phe Ser Ser Ser Pro His Ala Val Leu Thr Thr Asp Thr Ser	
70 75 80	
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Ser Glu Leu Ala Glu Lys Phe Ser Leu Gly Gly Asn Ile Glu Leu Gln	
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425 430 435	
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His Pro Gln Tyr Arg Glu Ile Leu Arg Met Ile Met Ser Thr Val Gly	
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CGT GGA GGT GAA GGG GAT GTA GGA CAG CGA ATT AGG GAT GAA ATT TTG	2132
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His Gln Lys Leu His Asn Asn Thr Ser Pro Asp Asp Val Val Ile Cys	
695 700 705	
CAG GCA TTA ATT GAC TAC ATC AAG AGT GAT TTT GAT CTT GGT GTT TAT	2276
Gln Ala Leu Ile Asp Tyr Ile Lys Ser Asp Phe Asp Leu Gly Val Tyr	
710 715 720	
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Tyr Asp Arg Ala Ile His Ser Glu Pro Asn Phe Arg Gly Asp Gln Lys	
745 750 755	

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Val	His	Ser	Gly	Ala	Asp	Leu	Glu	Ser	Ala	Ile	Ala	Asn	Cys	Met	Gly	
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TAC	AAA	ACT	GAG	GGA	GAA	GGC	TTT	ATG	GTT	GGA	GTC	CAG	ATA	AAT	CCT	2516
Tyr	Lys	Thr	Glu	Gly	Glu	Gly	Phe	Met	Val	Gly	Val	Gln	Ile	Asn	Pro	
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Leu	Lys	Asp	Leu	Leu	Phe	Leu	Asp	Ile	Ala	Leu	Asp	Ser	Thr	Val	Arg	
		855					860					865				
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Thr	Ala	Val	Glu	Arg	Gly	Tyr	Glu	Glu	Leu	Asn	Asn	Ala	Asn	Pro	Glu	
	870					875					880					
AAA	ATC	ATG	TAC	TTC	ATC	TCC	CTC	GTT	CTT	GAA	AAT	CTC	GCA	CTC	TCT	2804
Lys	Ile	Met	Tyr	Phe	Ile	Ser	Leu	Val	Leu	Glu	Asn	Leu	Ala	Leu	Ser	
	885				890					895					900	
GTG	GAC	GAT	AAT	GAA	GAT	CTT	GTT	TAT	TGC	TTG	AAG	GGA	TGG	AAT	CAA	2852
Val	Asp	Asp	Asn	Glu	Asp	Leu	Val	Tyr	Cys	Leu	Lys	Gly	Trp	Asn	Gln	
				905					910					915		
GCT	CTT	TCA	ATG	TCC	AAT	GGT	GGG	GAC	AAC	CAT	TGG	GCT	TTA	TTT	GCA	2900
Ala	Leu	Ser	Met	Ser	Asn	Gly	Gly	Asp	Asn	His	Trp	Ala	Leu	Phe	Ala	
			920					925					930			
AAA	GCT	GTG	CTT	GAC	AGA	ACC	CGT	CTT	GCA	CTT	GCA	AGC	AAG	GCA	GAG	2948
Lys	Ala	Val	Leu	Asp	Arg	Thr	Arg	Leu	Ala	Leu	Ala	Ser	Lys	Ala	Glu	
		935					940					945				
TGG	TAC	CAT	CAC	TTA	TTG	CAG	CCA	TCT	GCC	GAA	TAT	CTA	GGA	TCA	ATA	2996
Trp	Tyr	His	His	Leu	Leu	Gln	Pro	Ser	Ala	Glu	Tyr	Leu	Gly	Ser	Ile	
	950					955					960					
CTT	GGG	GTG	GAC	CAA	TGG	GCT	TTG	AAC	ATA	TTT	ACT	GAA	GAA	ATT	ATA	3044
Leu	Gly	Val	Asp	Gln	Trp	Ala	Leu	Asn	Ile	Phe	Thr	Glu	Glu	Ile	Ile	
	965				970					975					980	
CGT	GCT	GGA	TCA	GCA	GCT	TCA	TTA	TCC	TCT	CTT	CTT	AAT	AGA	CTC	GAT	3092
Arg	Ala	Gly	Ser	Ala	Ala	Ser	Leu	Ser	Ser	Leu	Leu	Asn	Arg	Leu	Asp	
			985						990					995		

CCC GTG CTT CGG AAA ACT GCA AAT CTA GGA AGT TGG CAG ATT ATC AGT Pro Val Leu Arg Lys Thr Ala Asn Leu Gly Ser Trp Gln Ile Ile Ser 1000 1005 1010	3140
CCA GTT GAA GCC GTT GGA TAT GTT GTC GTT GTG GAT GAG TTG CTT TCA Pro Val Glu Ala Val Gly Tyr Val Val Val Val Asp Glu Leu Leu Ser 1015 1020 1025	3188
GTT CAG AAT GAA ATC TAC GAG AAG CCC ACG ATC TTA GTA GCA AAA TCT Val Gln Asn Glu Ile Tyr Glu Lys Pro Thr Ile Leu Val Ala Lys Ser 1030 1035 1040	3236
GTT AAA GGA GAG GAG GAA ATT CCT GAT GGT GCT GTT GCC CTG ATA ACA Val Lys Gly Glu Glu Glu Ile Pro Asp Gly Ala Val Ala Leu Ile Thr 1045 1050 1055 1060	3284
CCA GAC ATG CCA GAT GTT CTT TCA CAT GTT TCT GTT CGA GCT AGA AAT Pro Asp Met Pro Asp Val Leu Ser His Val Ser Val Arg Ala Arg Asn 1065 1070 1075	3332
GGG AAG GTT TGC TTT GCT ACA TGC TTT GAT CCC AAT ATA TTG GCT GAC Gly Lys Val Cys Phe Ala Thr Cys Phe Asp Pro Asn Ile Leu Ala Asp 1080 1085 1090	3380
CTC CAA GCA AAG GAA GGA AGG ATT TTG CTC TTA AAG CCT ACA CCT TCA Leu Gln Ala Lys Glu Gly Arg Ile Leu Leu Leu Lys Pro Thr Pro Ser 1095 1100 1105	3428
GAC ATA ATC TAT AGT GAG GTG AAT GAG ATT GAG CTC CAA AGT TCA AGT Asp Ile Ile Tyr Ser Glu Val Asn Glu Ile Glu Leu Gln Ser Ser Ser 1110 1115 1120	3476
AAC TTG GTA GAA GCT GAA ACT TCA GCA ACA CTT AGA TTG GTG AAA AAG Asn Leu Val Glu Ala Glu Thr Ser Ala Thr Leu Arg Leu Val Lys Lys 1125 1130 1135 1140	3524
CAA TTT GGT GGT TGT TAC GCA ATA TCA GCA GAT GAA TTC ACA AGT GAA Gln Phe Gly Gly Cys Tyr Ala Ile Ser Ala Asp Glu Phe Thr Ser Glu 1145 1150 1155	3572
ATG GTT GGA GCT AAA TCA CGT AAT ATT GCA TAT CTG AAA GGA AAA GTG Met Val Gly Ala Lys Ser Arg Asn Ile Ala Tyr Leu Lys Gly Lys Val 1160 1165 1170	3620
CCT TCC TCG GTG GGA ATT CCT ACG TCA GTA GCT CTT CCA TTT GGA GTC Pro Ser Ser Val Gly Ile Pro Thr Ser Val Ala Leu Pro Phe Gly Val 1175 1180 1185	3668
TTT GAG AAA GTA CTT TCA GAC GAC ATA AAT CAG GGA GTG GCA AAA GAG Phe Glu Lys Val Leu Ser Asp Asp Ile Asn Gln Gly Val Ala Lys Glu 1190 1195 1200	3716
TTG CAA ATT CTG ATG AAA AAA CTA TCT GAA GGA GAC TTC AGC GCT CTT Leu Gln Ile Leu Met Lys Lys Leu Ser Glu Gly Asp Phe Ser Ala Leu 1205 1210 1215 1220	3764
GGT GAA ATT CGC ACA ACG GTT TTA GAT CTT TCA GCA CCA GCT CAA TTG Gly Glu Ile Arg Thr Thr Val Leu Asp Leu Ser Ala Pro Ala Gln Leu 1225 1230 1235	3812

GTC AAA GAG CTG AAG GAG AAG ATG CAG GGT TCT GGC ATG CCT TGG CCT 3860
Val Lys Glu Leu Lys Glu Lys Met Gln Gly Ser Gly Met Pro Trp Pro
1240 1245 1250

GGT GAT GAA GGT CCA AAG CGG TGG GAA CAA GCA TGG ATG GCC ATA AAA 3908
Gly Asp Glu Gly Pro Lys Arg Trp Glu Gln Ala Trp Met Ala Ile Lys
1255 1260 1265

AAG GTG TGG GCT TCA AAA TGG AAT GAG AGA GCA TAC TTC AGC ACA AGG 3956
Lys Val Trp Ala Ser Lys Trp Asn Glu Arg Ala Tyr Phe Ser Thr Arg
1270 1275 1280

AAG GTG AAA CTG GAT CAT GAC TAT CTG TGC ATG GCT GTC CTT GTT CAA 4004
Lys Val Lys Leu Asp His Asp Tyr Leu Cys Met Ala Val Leu Val Gln
1285 1290 1295 1300

GAA ATA ATA AAT GCT GAT TAT GCA TTT GTC ATT CAC ACA ACC AAC CCA 4052
Glu Ile Ile Asn Ala Asp Tyr Ala Phe Val Ile His Thr Thr Asn Pro
1305 1310 1315

TCT TCC GGA GAC GAC TCA GAA ATA TAT GCC GAG GTG GTC AGG GGC CTT 4100
Ser Ser Gly Asp Asp Ser Glu Ile Tyr Ala Glu Val Val Arg Gly Leu
1320 1325 1330

GGG GAA ACA CTT GTT GGA GCT TAT CCA GGA CGT GCT TTG AGT TTT ATC 4148
Gly Glu Thr Leu Val Gly Ala Tyr Pro Gly Arg Ala Leu Ser Phe Ile
1335 1340 1345

TGC AAG AAA AAG GAT CTC AAC TCT CCT CAA GTG TTA GGT TAC CCA AGC 4196
Cys Lys Lys Lys Asp Leu Asn Ser Pro Gln Val Leu Gly Tyr Pro Ser
1350 1355 1360

AAA CCG ATC GGC CTT TTC ATA AAA AGA TCT ATC ATC TTC CGA TCT GAT 4244
Lys Pro Ile Gly Leu Phe Ile Lys Arg Ser Ile Ile Phe Arg Ser Asp
1365 1370 1375 1380

TCC AAT GGG GAA GAT TTG GAA GGT TAT GCC GGT GCT GGC CTC TAC GAC 4292
Ser Asn Gly Glu Asp Leu Glu Gly Tyr Ala Gly Ala Gly Leu Tyr Asp
1385 1390 1395

AGT GTA CCA ATG GAT GAG GAG GAA AAA GTT GTA ATT GAT TAC TCT TCC 4340
Ser Val Pro Met Asp Glu Glu Glu Lys Val Val Ile Asp Tyr Ser Ser
1400 1405 1410

GAC CCA TTG ATA ACT GAT GGT AAC TTC CGC CAG ACA ATC CTG TCC AAC 4388
Asp Pro Leu Ile Thr Asp Gly Asn Phe Arg Gln Thr Ile Leu Ser Asn
1415 1420 1425

ATT GCT CGT GCT GGA CAT GCT ATC GAG GAG CTA TAT GGC TCT CCT CAA 4436
Ile Ala Arg Ala Gly His Ala Ile Glu Glu Leu Tyr Gly Ser Pro Gln
1430 1435 1440

GAC ATT GAG GGT GTA GTG AGG GAT GGA AAG ATT TAT GTC GTT CAG ACA 4484
Asp Ile Glu Gly Val Val Arg Asp Gly Lys Ile Tyr Val Val Gln Thr
1445 1450 1455 1460

AGA CCA CAG ATG T GATTATATTC TCGTTGTATG TTGTTTCAGAG AAGACCACAG 4537
Arg Pro Gln Met

ATGTGATCAT ATTCTCATTG TATCAGATCT GTGACCACTT ACCTGATACC TCCCATGAAG 4597

TTACCTGTAT GATTATACGT GATCCAAAGC CATCACATCA TGTTACCTT CAGCTATTGG 4657
 AGGAGAAGTG AGAAGTAGGA ATTGCAATAT GAGGAATAAT AAGAAAAACT TTGTAAAAGC 4717
 TAAATTAGCT GGGTATGATA TAGGGAGAAA TGTGTAAACA TTGTACTATA TATAGTATAT 4777
 ACACACGCAT TATGTATTGC ATTATGCACT GAATAATATC GCAGCATCAA AGAAGAAATC 4837
 CTTTGGGTGG TTTCAAAAA 4856

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1464 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Ser Asn Ser Leu Gly Asn Asn Leu Leu Tyr Gln Gly Phe Leu Thr
 1 5 10 15
 Ser Thr Val Leu Glu His Lys Ser Arg Ile Ser Pro Pro Cys Val Gly
 20 25 30
 Gly Asn Ser Leu Phe Gln Gln Gln Val Ile Ser Lys Ser Pro Leu Ser
 35 40 45
 Thr Glu Phe Arg Gly Asn Arg Leu Lys Val Gln Lys Lys Lys Ile Pro
 50 55 60
 Met Glu Lys Lys Arg Ala Phe Ser Ser Ser Pro His Ala Val Leu Thr
 65 70 75 80
 Thr Asp Thr Ser Ser Glu Leu Ala Glu Lys Phe Ser Leu Gly Gly Asn
 85 90 95
 Ile Glu Leu Gln Val Asp Val Arg Pro Pro Thr Ser Gly Asp Val Ser
 100 105 110
 Phe Val Asp Phe Gln Val Thr Asn Gly Ser Asp Lys Leu Phe Leu His
 115 120 125
 Trp Gly Ala Val Lys Phe Gly Lys Glu Thr Trp Ser Leu Pro Asn Asp
 130 135 140
 Arg Pro Asp Gly Thr Lys Val Tyr Lys Asn Lys Ala Leu Arg Thr Pro
 145 150 155 160
 Phe Val Lys Ser Gly Ser Asn Ser Ile Leu Arg Leu Glu Ile Arg Asp
 165 170 175
 Thr Ala Ile Glu Ala Ile Glu Phe Leu Ile Tyr Asp Glu Ala His Asp
 180 185 190
 Lys Trp Ile Lys Asn Asn Gly Gly Asn Phe Arg Val Lys Leu Ser Arg
 195 200 205
 Lys Glu Ile Arg Gly Pro Asp Val Ser Val Pro Glu Glu Leu Val Gln
 210 215 220

Ile Gln Ser Tyr Leu Arg Trp Glu Arg Lys Gly Lys Gln Asn Tyr Pro
 225 230 235 240
 Pro Glu Lys Glu Lys Glu Glu Tyr Glu Ala Ala Arg Thr Val Leu Gln
 245 250 255
 Glu Glu Ile Ala Arg Gly Ala Ser Ile Gln Asp Ile Arg Ala Arg Leu
 260 265 270
 Thr Lys Thr Asn Asp Lys Ser Gln Ser Lys Glu Glu Pro Leu His Val
 275 280 285
 Thr Lys Ser Asp Ile Pro Asp Asp Leu Ala Gln Ala Gln Ala Tyr Ile
 290 295 300
 Arg Trp Glu Lys Ala Gly Lys Pro Asn Tyr Pro Pro Glu Lys Gln Ile
 305 310 315 320
 Glu Glu Leu Glu Glu Ala Arg Arg Glu Leu Gln Leu Glu Leu Glu Lys
 325 330 335
 Gly Ile Thr Leu Asp Glu Leu Arg Lys Thr Ile Thr Lys Gly Glu Ile
 340 345 350
 Lys Thr Lys Val Glu Lys His Leu Lys Arg Ser Ser Phe Ala Val Glu
 355 360 365
 Arg Ile Gln Arg Lys Lys Arg Asp Phe Gly His Leu Ile Asn Lys Tyr
 370 375 380
 Thr Ser Ser Pro Ala Val Gln Val Gln Lys Val Leu Glu Glu Pro Pro
 385 390 395 400
 Ala Leu Ser Lys Ile Lys Leu Tyr Ala Lys Glu Lys Glu Glu Gln Ile
 405 410 415
 Asp Asp Pro Ile Leu Asn Lys Lys Ile Phe Lys Val Asp Asp Gly Glu
 420 425 430
 Leu Leu Val Leu Val Ala Lys Ser Ser Gly Lys Thr Lys Val His Leu
 435 440 445
 Ala Thr Asp Leu Asn Gln Pro Ile Thr Leu His Trp Ala Leu Ser Lys
 450 455 460
 Ser Pro Gly Glu Trp Met Val Pro Pro Ser Ser Ile Leu Pro Pro Gly
 465 470 475 480
 Ser Ile Ile Leu Asp Lys Ala Ala Glu Thr Pro Phe Ser Ala Ser Ser
 485 490 495
 Ser Asp Gly Leu Thr Ser Lys Val Gln Ser Leu Asp Ile Val Ile Glu
 500 505 510
 Asp Gly Asn Phe Val Gly Met Pro Phe Val Leu Leu Ser Gly Glu Lys
 515 520 525
 Trp Ile Lys Asn Gln Gly Ser Asp Phe Tyr Val Gly Phe Ser Ala Ala
 530 535 540

Ser Lys Leu Ala Leu Lys Ala Ala Gly Asp Gly Ser Gly Thr Ala Lys
 545 550 555 560
 Ser Leu Leu Asp Lys Ile Ala Asp Met Glu Ser Glu Ala Gln Lys Ser
 565 570 575
 Phe Met His Arg Phe Asn Ile Ala Ala Asp Leu Ile Glu Asp Ala Thr
 580 585 590
 Ser Ala Gly Glu Leu Gly Phe Ala Gly Ile Leu Val Trp Met Arg Phe
 595 600 605
 Met Ala Thr Arg Gln Leu Ile Trp Asn Lys Asn Tyr Asn Val Lys Pro
 610 615 620
 Arg Glu Ile Ser Lys Ala Gln Asp Arg Leu Thr Asp Leu Leu Gln Asn
 625 630 635 640
 Ala Phe Thr Ser His Pro Gln Tyr Arg Glu Ile Leu Arg Met Ile Met
 645 650 655
 Ser Thr Val Gly Arg Gly Gly Glu Gly Asp Val Gly Gln Arg Ile Arg
 660 665 670
 Asp Glu Ile Leu Val Ile Gln Arg Asn Asn Asp Cys Lys Gly Gly Met
 675 680 685
 Met Gln Glu Trp His Gln Lys Leu His Asn Asn Thr Ser Pro Asp Asp
 690 695 700
 Val Val Ile Cys Gln Ala Leu Ile Asp Tyr Ile Lys Ser Asp Phe Asp
 705 710 715 720
 Leu Gly Val Tyr Trp Lys Thr Leu Asn Glu Asn Gly Ile Thr Lys Glu
 725 730 735
 Arg Leu Leu Ser Tyr Asp Arg Ala Ile His Ser Glu Pro Asn Phe Arg
 740 745 750
 Gly Asp Gln Lys Gly Gly Leu Leu Arg Asp Leu Gly His Tyr Met Arg
 755 760 765
 Thr Leu Lys Ala Val His Ser Gly Ala Asp Leu Glu Ser Ala Ile Ala
 770 775 780
 Asn Cys Met Gly Tyr Lys Thr Glu Gly Glu Gly Phe Met Val Gly Val
 785 790 795 800
 Gln Ile Asn Pro Val Ser Gly Leu Pro Ser Gly Phe Gln Asp Leu Leu
 805 810 815
 His Phe Val Leu Asp His Val Glu Asp Lys Asn Val Glu Thr Leu Leu
 820 825 830
 Glu Arg Leu Leu Glu Ala Arg Glu Glu Leu Arg Pro Leu Leu Leu Lys
 835 840 845
 Pro Asn Asn Arg Leu Lys Asp Leu Leu Phe Leu Asp Ile Ala Leu Asp
 850 855 860
 Ser Thr Val Arg Thr Ala Val Glu Arg Gly Tyr Glu Glu Leu Asn Asn
 865 870 875 880

85

Ala Asn Pro Glu Lys Ile Met Tyr Phe Ile Ser Leu Val Leu Glu Asn
 885 890 895
 Leu Ala Leu Ser Val Asp Asp Asn Glu Asp Leu Val Tyr Cys Leu Lys
 900 905 910
 Gly Trp Asn Gln Ala Leu Ser Met Ser Asn Gly Gly Asp Asn His Trp
 915 920 925
 Ala Leu Phe Ala Lys Ala Val Leu Asp Arg Thr Arg Leu Ala Leu Ala
 930 935 940
 Ser Lys Ala Glu Trp Tyr His His Leu Leu Gln Pro Ser Ala Glu Tyr
 945 950 955 960
 Leu Gly Ser Ile Leu Gly Val Asp Gln Trp Ala Leu Asn Ile Phe Thr
 965 970 975
 Glu Glu Ile Ile Arg Ala Gly Ser Ala Ala Ser Leu Ser Ser Leu Leu
 980 985 990
 Asn Arg Leu Asp Pro Val Leu Arg Lys Thr Ala Asn Leu Gly Ser Trp
 995 1000 1005
 Gln Ile Ile Ser Pro Val Glu Ala Val Gly Tyr Val Val Val Val Asp
 1010 1015 1020
 Glu Leu Leu Ser Val Gln Asn Glu Ile Tyr Glu Lys Pro Thr Ile Leu
 1025 1030 1035 1040
 Val Ala Lys Ser Val Lys Gly Glu Glu Glu Ile Pro Asp Gly Ala Val
 1045 1050 1055
 Ala Leu Ile Thr Pro Asp Met Pro Asp Val Leu Ser His Val Ser Val
 1060 1065 1070
 Arg Ala Arg Asn Gly Lys Val Cys Phe Ala Thr Cys Phe Asp Pro Asn
 1075 1080 1085
 Ile Leu Ala Asp Leu Gln Ala Lys Glu Gly Arg Ile Leu Leu Leu Lys
 1090 1095 1100
 Pro Thr Pro Ser Asp Ile Ile Tyr Ser Glu Val Asn Glu Ile Glu Leu
 1105 1110 1115 1120
 Gln Ser Ser Ser Asn Leu Val Glu Ala Glu Thr Ser Ala Thr Leu Arg
 1125 1130 1135
 Leu Val Lys Lys Gln Phe Gly Gly Cys Tyr Ala Ile Ser Ala Asp Glu
 1140 1145 1150
 Phe Thr Ser Glu Met Val Gly Ala Lys Ser Arg Asn Ile Ala Tyr Leu
 1155 1160 1165
 Lys Gly Lys Val Pro Ser Ser Val Gly Ile Pro Thr Ser Val Ala Leu
 1170 1175 1180
 Pro Phe Gly Val Phe Glu Lys Val Leu Ser Asp Asp Ile Asn Gln Gly
 1185 1190 1195 1200
 Val Ala Lys Glu Leu Gln Ile Leu Met Lys Lys Leu Ser Glu Gly Asp
 1205 1210 1215

Phe Ser Ala Leu Gly Glu Ile Arg Thr Thr Val Leu Asp Leu Ser Ala
 1220 1225 1230
 Pro Ala Gln Leu Val Lys Glu Leu Lys Glu Lys Met Gln Gly Ser Gly
 1235 1240 1245
 Met Pro Trp Pro Gly Asp Glu Gly Pro Lys Arg Trp Glu Gln Ala Trp
 1250 1255 1260
 Met Ala Ile Lys Lys Val Trp Ala Ser Lys Trp Asn Glu Arg Ala Tyr
 1265 1270 1275 1280
 Phe Ser Thr Arg Lys Val Lys Leu Asp His Asp Tyr Leu Cys Met Ala
 1285 1290 1295
 Val Leu Val Gln Glu Ile Ile Asn Ala Asp Tyr Ala Phe Val Ile His
 1300 1305 1310
 Thr Thr Asn Pro Ser Ser Gly Asp Asp Ser Glu Ile Tyr Ala Glu Val
 1315 1320 1325
 Val Arg Gly Leu Gly Glu Thr Leu Val Gly Ala Tyr Pro Gly Arg Ala
 1330 1335 1340
 Leu Ser Phe Ile Cys Lys Lys Lys Asp Leu Asn Ser Pro Gln Val Leu
 1345 1350 1355 1360
 Gly Tyr Pro Ser Lys Pro Ile Gly Leu Phe Ile Lys Arg Ser Ile Ile
 1365 1370 1375
 Phe Arg Ser Asp Ser Asn Gly Glu Asp Leu Glu Gly Tyr Ala Gly Ala
 1380 1385 1390
 Gly Leu Tyr Asp Ser Val Pro Met Asp Glu Glu Glu Lys Val Val Ile
 1395 1400 1405
 Asp Tyr Ser Ser Asp Pro Leu Ile Thr Asp Gly Asn Phe Arg Gln Thr
 1410 1415 1420
 Ile Leu Ser Asn Ile Ala Arg Ala Gly His Ala Ile Glu Glu Leu Tyr
 1425 1430 1435 1440
 Gly Ser Pro Gln Asp Ile Glu Gly Val Val Arg Asp Gly Lys Ile Tyr
 1445 1450 1455
 Val Val Gln Thr Arg Pro Gln Met
 1460

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1918 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Solanum tuberosum*

(B) STRAIN: C.V. Desiree

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:1..1555

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GCA GAG TGG TAC CAT CAC TTA TTG CAG CCA TCT GCC GAA TAT CTA GGA	48
Ala Glu Trp Tyr His His Leu Leu Gln Pro Ser Ala Glu Tyr Leu Gly	
1 5 10 15	
TCA ATA CTT GGG GTG GAC CAA TGG GCT TTG AAC ATA TTT ACT GAA GAA	96
Ser Ile Leu Gly Val Asp Gln Trp Ala Leu Asn Ile Phe Thr Glu Glu	
20 25 30	
ATT ATA CGT GCT GGA TCA GCA GCT TCA TTA TCC TCT CTT CTT AAT AGA	144
Ile Ile Arg Ala Gly Ser Ala Ala Ser Leu Ser Ser Leu Leu Asn Arg	
35 40 45	
CTC GAT CCC GTG CTT CGG AAA ACT GCA AAT CTA GGA AGT TGG CAG ATT	192
Leu Asp Pro Val Leu Arg Lys Thr Ala Asn Leu Gly Ser Trp Gln Ile	
50 55 60	
ATC AGT CCA GTT GAA GCC GTT GGA TAT GTT GTC GTT GTG GAT GAG TTG	240
Ile Ser Pro Val Glu Ala Val Gly Tyr Val Val Val Val Asp Glu Leu	
65 70 75 80	
CTT TCA GTT CAG AAT GAA ATC TAC GAG AAG CCC ACG ATC TTA GTA GCA	288
Leu Ser Val Gln Asn Glu Ile Tyr Glu Lys Pro Thr Ile Leu Val Ala	
85 90 95	
AAA TCT GTT AAA GGA GAG GAG GAA ATT CCT GAT GGT GCT GTT GCC CTG	336
Lys Ser Val Lys Gly Glu Glu Glu Ile Pro Asp Gly Ala Val Ala Leu	
100 105 110	
ATA ACA CCA GAC ATG CCA GAT GTT CTT TCA CAT GTT TCT GTT CGA GCT	384
Ile Thr Pro Asp Met Pro Asp Val Leu Ser His Val Ser Val Arg Ala	
115 120 125	
AGA AAT GGG AAG GTT TGC TTT GCT ACA TGC TTT GAT CCC AAT ATA TTG	432
Arg Asn Gly Lys Val Cys Phe Ala Thr Cys Phe Asp Pro Asn Ile Leu	
130 135 140	
GCT GAC CTC CAA GCA AAG GAA GGA AGG ATT TTG CTC TTA AAG CCT ACA	480
Ala Asp Leu Gln Ala Lys Glu Gly Arg Ile Leu Leu Leu Lys Pro Thr	
145 150 155 160	
CCT TCA GAC ATA ATC TAT AGT GAG GTG AAT GAG ATT GAG CTC CAA AGT	528
Pro Ser Asp Ile Ile Tyr Ser Glu Val Asn Glu Ile Glu Leu Gln Ser	
165 170 175	
TCA AGT AAC TTG GTA GAA GCT GAA ACT TCA GCA ACA CTT AGA TTG GTG	576
Ser Ser Asn Leu Val Glu Ala Glu Thr Ser Ala Thr Leu Arg Leu Val	
180 185 190	
AAA AAG CAA TTT GGT GGT TGT TAC GCA ATA TCA GCA GAT GAA TTC ACA	624
Lys Lys Gln Phe Gly Gly Cys Tyr Ala Ile Ser Ala Asp Glu Phe Thr	
195 200 205	

AGT GAA ATG GTT GGA GCT AAA TCA CGT AAT ATT GCA TAT CTG AAA GGA Ser Glu Met Val Gly Ala Lys Ser Arg Asn Ile Ala Tyr Leu Lys Gly 210 215 220	672
AAA GTG CCT TCC TCG GTG GGA ATT CCT ACG TCA GTA GCT CTT CCA TTT Lys Val Pro Ser Ser Val Gly Ile Pro Thr Ser Val Ala Leu Pro Phe 225 230 235 240	720
GGA GTC TTT GAG AAA GTA CTT TCA GAC GAC ATA AAT CAG GGA GTG GCA Gly Val Phe Glu Lys Val Leu Ser Asp Asp Ile Asn Gln Gly Val Ala 245 250 255	768
AAA GAG TTG CAA ATT CTG ACA AAA AAA CTA TCT GAA GGA GAC TTT AGC Lys Glu Leu Gln Ile Leu Thr Lys Lys Leu Ser Glu Gly Asp Phe Ser 260 265 270	816
GCT CTT GGT GAA ATT CGC ACA ACG GTT TTA GAT CTT TCG ACA CCA GCT Ala Leu Gly Glu Ile Arg Thr Thr Val Leu Asp Leu Ser Thr Pro Ala 275 280 285	864
CAA TTG GTC AAA GAG CTG AAG GAG AAG ATG CAG GGT TCT GGC ATG CCT Gln Leu Val Lys Glu Leu Lys Glu Lys Met Gln Gly Ser Gly Met Pro 290 295 300	912
TGG CCT GGT GAT GAA GGT CCA AAG CGG TGG GAA CAA GCA TGG ATG GCC Trp Pro Gly Asp Glu Gly Pro Lys Arg Trp Glu Gln Ala Trp Met Ala 305 310 315 320	960
ATA AAA AAG GTG TGG GCT TCA AAA TGG AAT GAG AGA GCA TAC TTC AGC Ile Lys Lys Val Trp Ala Ser Lys Trp Asn Glu Arg Ala Tyr Phe Ser 325 330 335	1008
ACA AGG AAG GTG AAA CTG GAT CAT GAC TAT CTG TGC ATG GCT GTC CTT Thr Arg Lys Val Lys Leu Asp His Asp Tyr Leu Cys Met Ala Val Leu 340 345 350	1056
GTT CAA GAA ATA ATA AAT GCT GAT TAT GCA TTT GTC ATT CAC ACA ACC Val Gln Glu Ile Ile Asn Ala Asp Tyr Ala Phe Val Ile His Thr Thr 355 360 365	1104
AAC CCA TCT TCC GGA GAC GAC TCA GAA ATA TAT GCC GAG GTG GTC AGG Asn Pro Ser Ser Gly Asp Asp Ser Ser Glu Ile Tyr Ala Glu Val Val Arg 370 375 380	1152
GGC CTT GGG GAA ACA CTT GTT GGA GCT TAT CCA GGA CGT GCT TTG AGT Gly Leu Gly Glu Thr Leu Val Gly Ala Tyr Pro Gly Arg Ala Leu Ser 385 390 395 400	1200
TTT ATC TGC AAG AAA AAG GAT CTC AAC TCT CCT CAA GTG TTA GGT TAC Phe Ile Cys Lys Lys Lys Asp Leu Asn Ser Pro Gln Val Leu Gly Tyr 405 410 415	1248
CCA AGC AAA CCG ATC GGC CTT TTC ATA AAA AGA TCT ATC ATC TTC CGA Pro Ser Lys Pro Ile Gly Leu Phe Ile Lys Arg Ser Ile Ile Phe Arg 420 425 430	1296
TCT GAT TCC AAT GGG GAA GAT TTG GAA GGT TAT GCC GGT GCT GGC CTC Ser Asp Ser Asn Gly Glu Asp Leu Glu Gly Tyr Ala Gly Ala Gly Leu 435 440 445	1344

89

TAC GAC AGT GTA CCA ATG GAT GAG GAG GAA AAA GTT GTA ATT GAT TAC	1392
Tyr Asp Ser Val Pro Met Asp Glu Glu Glu Lys Val Val Ile Asp Tyr	
450 455 460	
TCT TCC GAC CCA TTG ATA ACT GAT GGT AAC TTC CGC CAG ACA ATC CTG	1440
Ser Ser Asp Pro Leu Ile Thr Asp Gly Asn Phe Arg Gln Thr Ile Leu	
465 470 475 480	
TCC AAC ATT GCT CGT GCT GGA CAT GCT ATC GAG GAG CTA TAT GGC TCT	1488
Ser Asn Ile Ala Arg Ala Gly His Ala Ile Glu Glu Leu Tyr Gly Ser	
485 490 495	
CCT CAA GAC ATT GAG GGT GTA GTG AGG GAT GGA AAG ATT TAT GTC GTT	1536
Pro Gln Asp Ile Glu Gly Val Val Arg Asp Gly Lys Ile Tyr Val Val	
500 505 510	
CAG ACA AGA CCA CAG ATG T GATTATATTC TCGTTGTATG TTGTTTCAGAG	1585
Gln Thr Arg Pro Gln Met	
515-	
AAGACCACAG ATGTGATCAT ATTCTCATTG TATCAGATCT GTGACCACTT ACCTGATACC	1645
TTCCATGAAG TTACCTGTAT GATTATACGT GATCCAAAGC CATCACATCA TGTTACCTT	1705
CAGCTATTGG AGGAGAAGTG AGAAGTAGGA ATTGCAATAT GAGGAATAAT AAGAAAAACT	1765
TTGTAAAAGC TAAATTAGCT GGGTATGATA TAGGGAGAAA TGTGTAAACA TTGTACTATA	1825
TATAGTATAT ACACACGCAT TATGTATTGC ATTATGCACT GAATAATATC GCAGCATCAA	1885
AGAAGAAATC CTTTGGGTGG TTTCAAAAAA AAA	1918

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 518 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Ala Glu Trp Tyr His His Leu Leu Gln Pro Ser Ala Glu Tyr Leu Gly	
1 5 10 15	
Ser Ile Leu Gly Val Asp Gln Trp Ala Leu Asn Ile Phe Thr Glu Glu	
20 25 30	
Ile Ile Arg Ala Gly Ser Ala Ala Ser Leu Ser Ser Leu Leu Asn Arg	
35 40 45	
Leu Asp Pro Val Leu Arg Lys Thr Ala Asn Leu Gly Ser Trp Gln Ile	
50 55 60	
Ile Ser Pro Val Glu Ala Val Gly Tyr Val Val Val Val Asp Glu Leu	
65 70 75 80	
Leu Ser Val Gln Asn Glu Ile Tyr Glu Lys Pro Thr Ile Leu Val Ala	
85 90 95	

Lys Ser Val Lys Gly Glu Glu Glu Ile Pro Asp Gly Ala Val Ala Leu
 100 105 110
 Ile Thr Pro Asp Met Pro Asp Val Leu Ser His Val Ser Val Arg Ala
 115 120 125
 Arg Asn Gly Lys Val Cys Phe Ala Thr Cys Phe Asp Pro Asn Ile Leu
 130 135 140
 Ala Asp Leu Gln Ala Lys Glu Gly Arg Ile Leu Leu Leu Lys Pro Thr
 145 150 155 160
 Pro Ser Asp Ile Ile Tyr Ser Glu Val Asn Glu Ile Glu Leu Gln Ser
 165 170 175
 Ser Ser Asn Leu Val Glu Ala Glu Thr Ser Ala Thr Leu Arg Leu Val
 180 185 190
 Lys Lys Gln Phe Gly Gly Cys Tyr Ala Ile Ser Ala Asp Glu Phe Thr
 195 200 205
 Ser Glu Met Val Gly Ala Lys Ser Arg Asn Ile Ala Tyr Leu Lys Gly
 210 215 220
 Lys Val Pro Ser Ser Val Gly Ile Pro Thr Ser Val Ala Leu Pro Phe
 225 230 235 240
 Gly Val Phe Glu Lys Val Leu Ser Asp Asp Ile Asn Gln Gly Val Ala
 245 250 255
 Lys Glu Leu Gln Ile Leu Thr Lys Lys Leu Ser Glu Gly Asp Phe Ser
 260 265 270
 Ala Leu Gly Glu Ile Arg Thr Thr Val Leu Asp Leu Ser Thr Pro Ala
 275 280 285
 Gln Leu Val Lys Glu Leu Lys Glu Lys Met Gln Gly Ser Gly Met Pro
 290 295 300
 Trp Pro Gly Asp Glu Gly Pro Lys Arg Trp Glu Gln Ala Trp Met Ala
 305 310 315 320
 Ile Lys Lys Val Trp Ala Ser Lys Trp Asn Glu Arg Ala Tyr Phe Ser
 325 330 335
 Thr Arg Lys Val Lys Leu Asp His Asp Tyr Leu Cys Met Ala Val Leu
 340 345 350
 Val Gln Glu Ile Ile Asn Ala Asp Tyr Ala Phe Val Ile His Thr Thr
 355 360 365
 Asn Pro Ser Ser Gly Asp Asp Ser Glu Ile Tyr Ala Glu Val Val Arg
 370 375 380
 Gly Leu Gly Glu Thr Leu Val Gly Ala Tyr Pro Gly Arg Ala Leu Ser
 385 390 395 400
 Phe Ile Cys Lys Lys Lys Asp Leu Asn Ser Pro Gln Val Leu Gly Tyr
 405 410 415
 Pro Ser Lys Pro Ile Gly Leu Phe Ile Lys Arg Ser Ile Ile Phe Arg
 420 425 430

Ser Asp Ser Asn Gly Glu Asp Leu Glu Gly Tyr Ala Gly Ala Gly Leu
 435 440 445

Tyr Asp Ser Val Pro Met Asp Glu Glu Glu Lys Val Val Ile Asp Tyr
 450 455 460

Ser Ser Asp Pro Leu Ile Thr Asp Gly Asn Phe Arg Gln Thr Ile Leu
 465 470 475 480

Ser Asn Ile Ala Arg Ala Gly His Ala Ile Glu Glu Leu Tyr Gly Ser
 485 490 495

Pro Gln Asp Ile Glu Gly Val Val Arg Asp Gly Lys Ile Tyr Val Val
 500 505 510

Gln Thr Arg Pro Gln Met
 515

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2307 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Zea mays

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 33..1943

(xi) SEQUENZBESCHREIBUNG: SEQ ID NO: 5:

TAGTGGATCC CCCCGGGCTG CAGGGAATTC GG CAC GAG CTT GAG GGG CTA TTG	53
His Glu Leu Glu Gly Leu Leu	
1 5	
GAA GCT CGA GTT GAA CTG CGC CCT TTG CTT CTT GAT TCG CGT GAA CGC	101
Glu Ala Arg Val Glu Leu Arg Pro Leu Leu Leu Asp Ser Arg Glu Arg	
10 15 20	
ATG AAA GAT CTT ATA TTT TTG GAC ATT GCT CTT GAT TCT ACC TTC AGG	149
Met Lys Asp Leu Ile Phe Leu Asp Ile Ala Leu Asp Ser Thr Phe Arg	
25 30 35	
ACA GCA ATT GAA AGG TCA TAT GAG GAG CTG AAT GAT GCA GCC CCA GAG	197
Thr Ala Ile Glu Arg Ser Tyr Glu Glu Leu Asn Asp Ala Ala Pro Glu	
40 45 50 55	

AAA ATA ATG TAC TTC ATC AGT CTT GTC CTT GAA AAT CTT GCG CTT TCA	245
Lys Ile Met Tyr Phe Ile Ser Leu Val Leu Glu Asn Leu Ala Leu Ser	
60 65 70	
ATT GAC GAC AAT GAA GAC ATC CTG TAT TGT TTA AAG GGA TGG AAC CAA	293
Ile Asp Asp Asn Glu Asp Ile Leu Tyr Cys Leu Lys Gly Trp Asn Gln	
75 80 85	
GCC TTG GAA ATG GCT AAG CAA AAA GAC GAC CAA TGG GCG CTC TAT GCT	341
Ala Leu Glu Met Ala Lys Gln Lys Asp Asp Gln Trp Ala Leu Tyr Ala	
90 95 100	
AAA GCA TTT CTT GAC AGA AAC AGA CTT GCC CTT GCG AGC AAG GGA GAA	389
Lys Ala Phe Leu Asp Arg Asn Arg Leu Ala Leu Ala Ser Lys Gly Glu	
105 110 115	
CAA TAC CAT AAT ATG ATG CAG CCC TCT GCT GAG TAT CTT GGC TCG TTA	437
Gln Tyr His Asn Met Met Gln Pro Ser Ala Glu Tyr Leu Gly Ser Leu	
120 125 130 135	
CTC AGC ATA GAC CAA TGG GCA GTC AAT ATC TTC ACA GAA GAA ATT ATA	485
Leu Ser Ile Asp Gln Trp Ala Val Asn Ile Phe Thr Glu Glu Ile Ile	
140 145 150	
CGC GGT GGA TCA GCT GCT ACT CTG TCT GCT CTT CTG AAC CGA TTT GAT	533
Arg Gly Gly Ser Ala Ala Thr Leu Ser Ala Leu Leu Asn Arg Phe Asp	
155 160 165	
CCT GTT TTA AGG AAT GTT GCT CAC CTC GGA AGT TGG CAG GTT ATA AGC	581
Pro Val Leu Arg Asn Val Ala His Leu Gly Ser Trp Gln Val Ile Ser	
170 175 180	
CCG GTT GAA GTA TCA GGT TAT GTG GTT GTG GTT GAT GAG TTA CTT GCT	629
Pro Val Glu Val Ser Gly Tyr Val Val Val Val Asp Glu Leu Leu Ala	
185 190 195	
GTC CAG AAC AAA TCT TAT GAT AAA CCA ACC ATC CTT GTG GCA AAG AGT	677
Val Gln Asn Lys Ser Tyr Asp Lys Pro Thr Ile Leu Val Ala Lys Ser	
200 205 210 215	
GTC AAG GGA GAG GAA GAA ATA CCA GAT GGA GTA GTT GGT GTA ATT ACA	725
Val Lys Gly Glu Glu Glu Ile Pro Asp Gly Val Val Gly Val Ile Thr	
220 225 230	
CCT GAT ATG CCA GAT GTT CTG TCT CAT GTG TCA GTC CGA GCA AGG AAT	773
Pro Asp Met Pro Asp Val Leu Ser His Val Ser Val Arg Ala Arg Asn	
235 240 245	
AGC AAG GTA CTG TTT GCG ACC TGT TTT GAC CAC ACC ACT CTA TCT GAA	821
Ser Lys Val Leu Phe Ala Thr Cys Phe Asp His Thr Thr Leu Ser Glu	
250 255 260	
CTT GAA GGA TAT GAT CAG AAA CTG TTT TCC TTC AAG CCT ACT TCT GCA	869
Leu Glu Gly Tyr Asp Gln Lys Leu Phe Ser Phe Lys Pro Thr Ser Ala	
265 270 275	
GAT ATA ACC TAT AGG GAG ATC ACA GAG AGT GAA CTT CAG CAA TCA AGT	917
Asp Ile Thr Tyr Arg Glu Ile Thr Glu Ser Glu Leu Gln Gln Ser Ser	
280 285 290 295	

TCT	CCA	AAT	GCA	GAA	GTT	GGC	CAT	GCA	GTA	CCA	TCT	ATT	TCA	TTG	GCC	965
Ser	Pro	Asn	Ala	Glu	Val	Gly	His	Ala	Val	Pro	Ser	Ile	Ser	Leu	Ala	
				300					305					310		
AAG	AAG	AAA	TTT	CTT	GGA	AAA	TAT	GCA	ATA	TCA	GCC	GAA	GAA	TTC	TCT	1013
Lys	Lys	Lys	Phe	Leu	Gly	Lys	Tyr	Ala	Ile	Ser	Ala	Glu	Glu	Phe	Ser	
			315					320					325			
GAG	GAA	ATG	GTT	GGG	GCC	AAG	TCT	CGG	AAT	ATA	GCA	TAC	CTC	AAA	GGA	1061
Glu	Glu	Met	Val	Gly	Ala	Lys	Ser	Arg	Asn	Ile	Ala	Tyr	Leu	Lys	Gly	
		330					335					340				
AAA	GTA	CCT	TCA	TGG	GTC	GGT	GTC	CCA	ACG	TCA	GTT	GCG	ATA	CCA	TTT	1109
Lys	Val	Pro	Ser	Trp	Val	Gly	Val	Pro	Thr	Ser	Val	Ala	Ile	Pro	Phe	
		345				350					355					
GGC	ACT	TTT	GAG	AAG	GTT	TTG	TCA	GAT	GGG	CTT	AAT	AAG	GAA	GTA	GCA	1157
Gly	Thr	Phe	Glu	Lys	Val	Leu	Ser	Asp	Gly	Leu	Asn	Lys	Glu	Val	Ala	
360				365					370						375	
CAG	AGC	ATA	GAG	AAG	CTT	AAG	ATC	AGA	CTT	GCC	CAA	GAA	GAT	TTT	AGT	1205
Gln	Ser	Ile	Glu	Lys	Leu	Lys	Ile	Arg	Leu	Ala	Gln	Glu	Asp	Phe	Ser	
			380					385						390		
GCT	CTA	GGT	GAA	ATA	AGA	AAA	GTC	GTC	CTT	AAT	CTT	ACT	GCT	CCT	ATG	1253
Ala	Leu	Gly	Glu	Ile	Arg	Lys	Val	Val	Leu	Asn	Leu	Thr	Ala	Pro	Met	
		395					400					405				
CAA	TTG	GTT	AAT	GAG	CTG	AAG	GAG	AGG	ATG	CTA	GGC	TCT	GGA	ATG	CCC	1301
Gln	Leu	Val	Asn	Glu	Leu	Lys	Glu	Arg	Met	Leu	Gly	Ser	Gly	Met	Pro	
		410					415					420				
TGG	CCT	GGT	GAT	GAA	GGA	GAC	AAG	CGT	TGG	GAG	CAA	GCA	TGG	ATG	GCT	1349
Trp	Pro	Gly	Asp	Glu	Gly	Asp	Lys	Arg	Trp	Glu	Gln	Ala	Trp	Met	Ala	
	425					430					435					
ATT	AAA	AAG	GTT	TGG	GCA	TCA	AAA	TGG	AAC	GAA	AGA	GCA	TAT	TTT	AGC	1397
Ile	Lys	Lys	Val	Trp	Ala	Ser	Lys	Trp	Asn	Glu	Arg	Ala	Tyr	Phe	Ser	
440					445				450						455	
ACA	CGC	AAG	GTG	AAA	CTT	GAT	CAT	GAG	TAC	CTT	TCG	ATG	GCT	GTT	CTC	1445
Thr	Arg	Lys	Val	Lys	Leu	Asp	His	Glu	Tyr	Leu	Ser	Met	Ala	Val	Leu	
			460					465						470		
GTG	CAA	GAA	GTT	GTG	AAT	GCA	GAT	TAT	GCT	TTT	GTC	ATT	CAT	ACC	ACA	1493
Val	Gln	Glu	Val	Val	Asn	Ala	Asp	Tyr	Ala	Phe	Val	Ile	His	Thr	Thr	
		475					480					485				
AAC	CCA	TCG	TCT	GGA	GAT	TCT	TCT	GAG	ATA	TAT	GCT	GAA	GTG	GTG	AAA	1541
Asn	Pro	Ser	Ser	Gly	Asp	Ser	Ser	Glu	Ile	Tyr	Ala	Glu	Val	Val	Lys	
		490					495					500				
GGG	CTT	GGC	GAG	ACC	CTC	GTG	GGA	GCC	TAT	CCT	GGT	CGT	GCT	ATG	AGC	1589
Gly	Leu	Gly	Glu	Thr	Leu	Val	Gly	Ala	Tyr	Pro	Gly	Arg	Ala	Met	Ser	
	505					510					515					
TTT	GTT	TGC	AAA	AAA	GAT	GAC	CTT	GAC	TCT	CCC	AAG	TTA	CTT	GGT	TAC	1637
Phe	Val	Cys	Lys	Lys	Asp	Asp	Leu	Asp	Ser	Pro	Lys	Leu	Leu	Gly	Tyr	
520					525				530						535	

CCA AGC AAG CCA ATT GGT CTC TTC ATA AGG CAA TCA ATC ATC TTC CGT	1685
Pro Ser Lys Pro Ile Gly Leu Phe Ile Arg Gln Ser Ile Ile Phe Arg	
540 545 550	
TCC GAC TCC AAC GGT GAG GAC CTG GAA GGT TAT GCT GGA GCA GGA TTA	1733
Ser Asp Ser Asn Gly Glu Asp Leu Glu Gly Tyr Ala Gly Ala Gly Leu	
555 560 565	
TAT GAT AGT GTA CCG ATG GAT GAG GAG GAT GAG GTT GTA CTT GAT TAT	1781
Tyr Asp Ser Val Pro Met Asp Glu Glu Asp Glu Val Val Leu Asp Tyr	
570 575 580	
ACA ACT GAC CCT CTT ATA GTA GAC CGT GGA TTC CGA AGC TCA ATC CTC	1829
Thr Thr Asp Pro Leu Ile Val Asp Arg Gly Phe Arg Ser Ser Ile Leu	
585 590 595	
TCA AGC ATA GCA CGG GCT GGC CAT GCC ATC GAG GAG CTA TAT GGT TCT	1877
Ser Ser Ile Ala Arg Ala Gly His Ala Ile Glu Glu Leu Tyr Gly Ser	
600 605 610 615	
CCT CAG GAC GTC GAG GGA GTA GTG AAG GAT GGA AAA ATC TAT GTA GTC	1925
Pro Gln Asp Val Glu Gly Val Val Lys Asp Gly Lys Ile Tyr Val Val	
620 625 630	
CAG ACA AGA CCA CAG ATG TAGTATGTAT GCATCTATTA GACAGCTCAA	1973
Gln Thr Arg Pro Gln Met	
635	
TAAGCACTGT TGTACGCTTG TATGGTTGGG ACATATGGGC GTTATGGCAT GTATAGTTGT	2033
ATGCCTAGAT GTACAACACG TGTACTCGTA TATATATATA TAAATGCTGA AACAAGCATT	2093
GGTCCTGTAC TGTAGTTTCT ACATTTTCATT GTCACCAATA ATTAAGTGTA CTCCTATGGC	2153
TGGGAGTCTA TGAAATGGA CGTGTGACT TATTGGGTAA TAAATAATTT ATATATAAAA	2213
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA CTCGAGGGGG	2273
GGCCGGTCCC AATTCGCCTA TAGTGAGTCG TATA	2307

(2) ANGABEN ZU SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 637 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

His	Glu	Leu	Glu	Gly	Leu	Leu	Glu	Ala	Arg	Val	Glu	Leu	Arg	Pro	Leu
1				5					10					15	
Leu	Leu	Asp	Ser	Arg	Glu	Arg	Met	Lys	Asp	Leu	Ile	Phe	Leu	Asp	Ile
		20						25					30		
Ala	Leu	Asp	Ser	Thr	Phe	Arg	Thr	Ala	Ile	Glu	Arg	Ser	Tyr	Glu	Glu
		35					40					45			
Leu	Asn	Asp	Ala	Ala	Pro	Glu	Lys	Ile	Met	Tyr	Phe	Ile	Ser	Leu	Val
	50						55					60			

Leu Glu Asn Leu Ala Leu Ser Ile Asp Asp Asn Glu Asp Ile Leu Tyr
 65 70 75 80
 Cys Leu Lys Gly Trp Asn Gln Ala Leu Glu Met Ala Lys Gln Lys Asp
 85 90 95
 Asp Gln Trp Ala Leu Tyr Ala Lys Ala Phe Leu Asp Arg Asn Arg Leu
 100 105 110
 Ala Leu Ala Ser Lys Gly Glu Gln Tyr His Asn Met Met Gln Pro Ser
 115 120 125
 Ala Glu Tyr Leu Gly Ser Leu Leu Ser Ile Asp Gln Trp Ala Val Asn
 130 135 140
 Ile Phe Thr Glu Glu Ile Ile Arg Gly Gly Ser Ala Ala Thr Leu Ser
 145 150 155 160
 Ala Leu Leu Asn Arg Phe Asp Pro Val Leu Arg Asn Val Ala His Leu
 165 170 175
 Gly Ser Trp Gln Val Ile Ser Pro Val Glu Val Ser Gly Tyr Val Val
 180 185 190
 Val Val Asp Glu Leu Leu Ala Val Gln Asn Lys Ser Tyr Asp Lys Pro
 195 200 205
 Thr Ile Leu Val Ala Lys Ser Val Lys Gly Glu Glu Glu Ile Pro Asp
 210 215 220
 Gly Val Val Gly Val Ile Thr Pro Asp Met Pro Asp Val Leu Ser His
 225 230 235 240
 Val Ser Val Arg Ala Arg Asn Ser Lys Val Leu Phe Ala Thr Cys Phe
 245 250 255
 Asp His Thr Thr Leu Ser Glu Leu Glu Gly Tyr Asp Gln Lys Leu Phe
 260 265 270
 Ser Phe Lys Pro Thr Ser Ala Asp Ile Thr Tyr Arg Glu Ile Thr Glu
 275 280 285
 Ser Glu Leu Gln Gln Ser Ser Ser Pro Asn Ala Glu Val Gly His Ala
 290 295 300
 Val Pro Ser Ile Ser Leu Ala Lys Lys Lys Phe Leu Gly Lys Tyr Ala
 305 310 315 320
 Ile Ser Ala Glu Glu Phe Ser Glu Glu Met Val Gly Ala Lys Ser Arg
 325 330 335
 Asn Ile Ala Tyr Leu Lys Gly Lys Val Pro Ser Trp Val Gly Val Pro
 340 345 350
 Thr Ser Val Ala Ile Pro Phe Gly Thr Phe Glu Lys Val Leu Ser Asp
 355 360 365
 Gly Leu Asn Lys Glu Val Ala Gln Ser Ile Glu Lys Leu Lys Ile Arg
 370 375 380

96

Leu Ala Gln Glu Asp Phe Ser Ala Leu Gly Glu Ile Arg Lys Val Val
 385 390 395 400
 Leu Asn Leu Thr Ala Pro Met Gln Leu Val Asn Glu Leu Lys Glu Arg
 405 410 415
 Met Leu Gly Ser Gly Met Pro Trp Pro Gly Asp Glu Gly Asp Lys Arg
 420 425 430
 Trp Glu Gln Ala Trp Met Ala Ile Lys Lys Val Trp Ala Ser Lys Trp
 435 440 445
 Asn Glu Arg Ala Tyr Phe Ser Thr Arg Lys Val Lys Leu Asp His Glu
 450 455 460
 Tyr Leu Ser Met Ala Val Leu Val Gln Glu Val Val Asn Ala Asp Tyr
 465 470 475 480
 Ala Phe Val Ile His Thr Thr Asn Pro Ser Ser Gly Asp Ser Ser Glu
 485 490 495
 Ile Tyr Ala Glu Val Val Lys Gly Leu Gly Glu Thr Leu Val Gly Ala
 500 505 510
 Tyr Pro Gly Arg Ala Met Ser Phe Val Cys Lys Lys Asp Asp Leu Asp
 515 520 525
 Ser Pro Lys Leu Leu Gly Tyr Pro Ser Lys Pro Ile Gly Leu Phe Ile
 530 535 540
 Arg Gln Ser Ile Ile Phe Arg Ser Asp Ser Asn Gly Glu Asp Leu Glu
 545 550 555 560
 Gly Tyr Ala Gly Ala Gly Leu Tyr Asp Ser Val Pro Met Asp Glu Glu
 565 570 575
 Asp Glu Val Val Leu Asp Tyr Thr Thr Asp Pro Leu Ile Val Asp Arg
 580 585 590
 Gly Phe Arg Ser Ser Ile Leu Ser Ser Ile Ala Arg Ala Gly His Ala
 595 600 605
 Ile Glu Glu Leu Tyr Gly Ser Pro Gln Asp Val Glu Gly Val Val Lys
 610 615 620
 Asp Gly Lys Ile Tyr Val Val Gln Thr Arg Pro Gln Met
 625 630 635

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Zea mays*

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..4009

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

C	CCA	GAT	GGC	ACG	ACA	GTG	TAC	AAG	AAC	AGG	GCT	CTC	AGG	ACA	CCT	46
Pro	Asp	Gly	Thr	Thr	Val	Tyr	Lys	Asn	Arg	Ala	Leu	Arg	Thr	Pro		
1					5					10					15	
TTT	GTA	AAG	TCA	GGT	GAT	AAC	TCC	ACT	CTA	AGG	ATT	GAG	ATA	GAT	GAT	94
Phe	Val	Lys	Ser	Gly	Asp	Asn	Ser	Thr	Leu	Arg	Ile	Glu	Ile	Asp	Asp	
				20						25					30	
CCT	GGG	GTG	CAC	GCC	ATT	GAG	TTC	CTC	ATC	TTT	GAC	GAG	ACA	CAG	AAC	142
Pro	Gly	Val	His	Ala	Ile	Glu	Phe	Leu	Ile	Phe	Asp	Glu	Thr	Gln	Asn	
			35						40					45		
AAA	TGG	TTT	AAA	AAC	AAT	GGC	CAG	AAT	TTT	CAG	GTT	CAG	TTC	CAG	TCG	190
Lys	Trp	Phe	Lys	Asn	Asn	Gly	Gln	Asn	Phe	Gln	Val	Gln	Phe	Gln	Ser	
		50					55					60				
AGC	CGC	CAT	CAG	GGT	ACT	GGT	GCA	TCT	GGT	GCC	TCC	TCT	TCT	GCT	ACT	238
Ser	Arg	His	Gln	Gly	Thr	Gly	Ala	Ser	Gly	Ala	Ser	Ser	Ser	Ala	Thr	
		65				70					75					
TCT	ACC	TTG	GTG	CCA	GAG	GAT	CTT	GTG	CAG	ATC	CAA	GCT	TAC	CTT	CGG	286
Ser	Thr	Leu	Val	Pro	Glu	Asp	Leu	Val	Gln	Ile	Gln	Ala	Tyr	Leu	Arg	
	80					85				90					95	
TGG	GAA	AGA	AGG	GGA	AAG	CAG	TCA	TAC	ACA	CCA	GAG	CAA	GAA	AAG	GAG	334
Trp	Glu	Arg	Arg	Gly	Lys	Gln	Ser	Tyr	Thr	Pro	Glu	Gln	Glu	Lys	Glu	
				100					105					110		
GAG	TAT	GAA	GCT	GCA	CGA	GCT	GAG	TTA	ATA	GAG	GAA	GTA	AAC	AGA	GGT	382
Glu	Tyr	Glu	Ala	Ala	Arg	Ala	Glu	Leu	Ile	Glu	Glu	Val	Asn	Arg	Gly	
			115					120					125			
GTT	TCT	TTA	GAG	AAG	CTT	CGA	GCT	AAA	TTG	ACA	AAA	GCA	CCT	GAA	GCA	430
Val	Ser	Leu	Glu	Lys	Leu	Arg	Ala	Lys	Leu	Thr	Lys	Ala	Pro	Glu	Ala	
		130					135					140				
CCC	GAG	TCG	GAT	GAA	AGT	AAA	TCT	TCT	GCA	TCT	CGA	GTG	CCC	ATC	GGT	478
Pro	Glu	Ser	Asp	Glu	Ser	Lys	Ser	Ser	Ala	Ser	Arg	Val	Pro	Ile	Gly	
	145					150					155					
AAA	CTT	CCA	GAG	GAT	CTT	GTA	CAG	GTG	CAG	GCT	TAT	ATA	AGG	TGG	GAG	526
Lys	Leu	Pro	Glu	Asp	Leu	Val	Gln	Val	Gln	Ala	Tyr	Ile	Arg	Trp	Glu	
	160				165					170					175	
CAA	GCG	GGC	AAA	CCA	AAC	TAT	CCT	CCT	GAG	AAG	CAA	CTG	GTA	GAA	TTT	574
Gln	Ala	Gly	Lys	Pro	Asn	Tyr	Pro	Pro	Glu	Lys	Gln	Leu	Val	Glu	Phe	
				180					185					190		
GAG	GAA	GCA	AGG	AAG	GAA	CTG	CAG	GCT	GAG	GTG	GAC	AAG	GGA	ATC	TCT	622
Glu	Glu	Ala	Arg	Lys	Glu	Leu	Gln	Ala	Glu	Val	Asp	Lys	Gly	Ile	Ser	
			195					200					205			

ATT GAT CAG TTG AGG CAG AAA ATT TTG AAA GGA AAC ATT GAG AGT AAA Ile Asp Gln Leu Arg Gln Lys Ile Leu Lys Gly Asn Ile Glu Ser Lys 210 215 220	670
GTT TCC AAG CAG CTG AAG AAC AAG AAG TAC TTC TCT GTA GAA AGG ATT Val Ser Lys Gln Leu Lys Asn Lys Lys Tyr Phe Ser Val Glu Arg Ile 225 230 235	718
CAG CGC AAA AAG AGA GAT ATC ACA CAA CTT CTC AGT AAA CAT AAG CAT Gln Arg Lys Lys Arg Asp Ile Thr Gln Leu Leu Ser Lys His Lys His 240 245 250 255	766
ACA GTT ATG GAA GAT AAA GTA GAG GTT GTA CCA AAA CAA CCA ACT GTT Thr Val Met Glu Asp Lys Val Glu Val Val Pro Lys Gln Pro Thr Val 260 265 270	814
CTT GAT CTC TTC ACC AAG TCT TTA CAT GAG AAG GAT GGC TGT GAA GTT Leu Asp Leu Phe Thr Lys Ser Leu His Glu Lys Asp Gly Cys Glu Val 275 280 285	862
CTA AGC AGA AAG CTC TTC AAG TTC GGC GAT AAA GAG ATA CTG GCA ATT Leu Ser Arg Lys Leu Phe Lys Phe Gly Asp Lys Glu Ile Leu Ala Ile 290 295 300	910
TCT ACC AAG GTT CAA AAT AAA ACA GAA GTT CAC TTG GCA ACA AAC CAT Ser Thr Lys Val Gln Asn Lys Thr Glu Val His Leu Ala Thr Asn His 305 310 315	958
ACG GAC CCA CTT ATT CTT CAC TGG TCT TTG GCA AAA AAT GCT GGA GAA Thr Asp Pro Leu Ile Leu His Trp Ser Leu Ala Lys Asn Ala Gly Glu 320 325 330 335	1006
TGG AAG GCA CCT TCT CCA AAT ATA TTG CCA TCT GGT TCC ACA TTG CTG Trp Lys Ala Pro Ser Pro Asn Ile Leu Pro Ser Gly Ser Thr Leu Leu 340 345 350	1054
GAC AAG GCG TGT GAA ACT GAA TTT ACT AAA TCT GAA TTG GAT GGT TTG Asp Lys Ala Cys Glu Thr Glu Phe Thr Lys Ser Glu Leu Asp Gly Leu 355 360 365	1102
CAT TAC CAG GTT GTT GAG ATA GAG CTT GAT GAC GGA GGA TAC AAA GGA His Tyr Gln Val Val Glu Ile Glu Leu Asp Asp Gly Gly Tyr Lys Gly 370 375 380	1150
ATG CCA TTT GTT CTT CGG TCT GGT GAA ACA TGG ATA AAA AAT AAT GGT Met Pro Phe Val Leu Arg Ser Gly Glu Thr Trp Ile Lys Asn Asn Gly 385 390 395	1198
TCT GAT TTT TTC CTA GAT TTC AGC ACC CAT GAT GTC AGA AAT ATT AAG Ser Asp Phe Phe Leu Asp Phe Ser Thr His Asp Val Arg Asn Ile Lys 400 405 410 415	1246
GCA ATT TTA AAG GAC AAT GGC GAT GCT GGT AAA GGT ACT TCT AAG GCG Ala Ile Leu Lys Asp Asn Gly Asp Ala Gly Lys Gly Thr Ser Lys Ala 420 425 430	1294
TTG CTG GAG AGA ATA GCA GAT CTG GAG GAA GAT GCC CAG CGA TCT CTT Leu Leu Glu Arg Ile Ala Asp Leu Glu Glu Asp Ala Gln Arg Ser Leu 435 440 445	1342

ATG CAC AGA TTC AAT ATT GCA GCA GAT CTA GCT GAC CAA GCC AGA GAT Met His Arg Phe Asn Ile Ala Ala Asp Leu Ala Asp Gln Ala Arg Asp 450 455 460	1390
GCT GGA CTT TTG GGT ATT GTT GGG CTT TTT GTT TGG ATT AGA TTC ATG Ala Gly Leu Leu Gly Ile Val Gly Leu Phe Val Trp Ile Arg Phe Met 465 470 475	1438
GCT ACC AGG CAA CTA ACA TGG AAT AAG AAC TAT AAT GTG AAG CCA CGT Ala Thr Arg Gln Leu Thr Trp Asn Lys Asn Tyr Asn Val Lys Pro Arg 480 485 490 495	1486
GAG ATA AGC AAA GCA CAG GAT AGG TTT ACA GAT GAT CTT GAG AAT ATG Glu Ile Ser Lys Ala Gln Asp Arg Phe Thr Asp Asp Leu Glu Asn Met 500 505 510	1534
TAC AAA ACT TAT CCA CAG TAC AGA GAG ATA TTA AGA ATG ATA ATG GCT Tyr Lys Thr Tyr Pro Gln Tyr Arg Glu Ile Leu Arg Met Ile Met Ala 515 520 525	1582
GCT GTT GGT CGC GGA GGT GAA GGT GAT GTT GGT CAA CGC ATT CGT GAT Ala Val Gly Arg Gly Gly Glu Gly Asp Val Gly Gln Arg Ile Arg Asp 530 535 540	1630
GAG ATA TTA GTA ATA CAG AGA AAT AAT GAC TGC AAA GGT GGA ATG ATG Glu Ile Leu Val Ile Gln Arg Asn Asn Asp Cys Lys Gly Gly Met Met 545 550 555	1678
GAA GAA TGG CAC CAG AAA TTG CAC AAC AAT ACA AGC CCA GAT GAT GTA Glu Glu Trp His Gln Lys Leu His Asn Asn Thr Ser Pro Asp Asp Val 560 565 570 575	1726
GTG ATA TGC CAG GCC TTA ATT GAT TAT ATC AAG AGT GAC TTT GAT ATA Val Ile Cys Gln Ala Leu Ile Asp Tyr Ile Lys Ser Asp Phe Asp Ile 580 585 590	1774
AGC GTT TAC TGG GAC ACC TTG AAC AAA AAT GGC ATA ACC AAA GAG CGT Ser Val Tyr Trp Asp Thr Leu Asn Lys Asn Gly Ile Thr Lys Glu Arg 595 600 605	1822
CTC TTG AGC TAT GAT CGT GCT ATT CAT TCA GAA CCA AAT TTC AGA AGT Leu Leu Ser Tyr Asp Arg Ala Ile His Ser Glu Pro Asn Phe Arg Ser 610 615 620	1870
GAA CAG AAG GCG GGT TTA CTC CGT GAC CTG GGA AAT TAC ATG AGA AGC Glu Gln Lys Ala Gly Leu Leu Arg Asp Leu Gly Asn Tyr Met Arg Ser 625 630 635	1918
CTA AAG GCT GTG CAT TCT GGT GCT GAT CTT GAA TCT GCT ATA GCA AGT Leu Lys Ala Val His Ser Gly Ala Asp Leu Glu Ser Ala Ile Ala Ser 640 645 650 655	1966
TGT ATG GGA TAC AAA TCA GAG GGT GAA GGT TTC ATG GTT GGT GTT CAG Cys Met Gly Tyr Lys Ser Glu Gly Glu Gly Phe Met Val Gly Val Gln 660 665 670	2014
ATC AAT CCA GTG AAG GGT TTA CCA TCT GGA TTT CCG GAG TTG CTT GAA Ile Asn Pro Val Lys Gly Leu Pro Ser Gly Phe Pro Glu Leu Leu Glu 675 680 685	2062

100

TTT GTG CTT GAA CAT GTT GAG GAT AAA TCA GCG GAA CCA CTT CCT GAG	2110
Phe Val Leu Glu His Val Glu Asp Lys Ser Ala Glu Pro Leu Pro Glu	
690 695 700	
GGG CTA TTG GAA GCT CGA GTT GAA CTG CGC CCT TTG CTT CTT GAT TCG	2158
Gly Leu Leu Glu Ala Arg Val Glu Leu Arg Pro Leu Leu Leu Asp Ser	
705 710 715	
CGT GAA CGC ATG AAA GAT CTT ATA TTT TTG GAC ATT GCT CTT GAT TCT	2206
Arg Glu Arg Met Lys Asp Leu Ile Phe Leu Asp Ile Ala Leu Asp Ser	
720 725 730 735	
ACC TTC AGG ACA GCA ATT GAA AGG TCA TAT GAG GAG CTG AAT GAT GCA	2254
Thr Phe Arg Thr Ala Ile Glu Arg Ser Tyr Glu Glu Leu Asn Asp Ala	
740 745 750	
GCC CCA GAG AAA ATA ATG TAC TTC ATC AGT CTT GTC CTT GAA AAT CTT	2302
Ala Pro Glu Lys Ile Met Tyr Phe Ile Ser Leu Val Leu Glu Asn Leu	
755 760 765	
GCG CTT TCA ATT GAC GAC AAT GAA GAC ATC CTG TAT TGT TTA AAG GGA	2350
Ala Leu Ser Ile Asp Asp Asn Glu Asp Ile Leu Tyr Cys Leu Lys Gly	
770 775 780	
TGG AAC CAA GCC TTG GAA ATG GCT AAG CAA AAA GAC GAC CAA TGG GCG	2398
Trp Asn Gln Ala Leu Glu Met Ala Lys Gln Lys Asp Asp Gln Trp Ala	
785 790 795	
CTC TAT GCT AAA GCA TTT CTT GAC AGA AAC AGA CTT GCC CTT GCG AGC	2446
Leu Tyr Ala Lys Ala Phe Leu Asp Arg Asn Arg Leu Ala Leu Ala Ser	
800 805 810 815	
AAG GGA GAA CAA TAC CAT AAT ATG ATG CAG CCC TCT GCT GAG TAT CTT	2494
Lys Gly Glu Gln Tyr His Asn Met Met Gln Pro Ser Ala Glu Tyr Leu	
820 825 830	
GGC TCG TTA CTC AGC ATA GAC CAA TGG GCA GTC AAT ATC TTC ACA GAA	2542
Gly Ser Leu Leu Ser Ile Asp Gln Trp Ala Val Asn Ile Phe Thr Glu	
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GAA ATT ATA CGC GGT GGA TCA GCT GCT ACT CTG TCT GCT CTT CTG AAC	2590
Glu Ile Ile Arg Gly Gly Ser Ala Ala Thr Leu Ser Ala Leu Leu Asn	
850 855 860	
CGA TTT GAT CCT GTT TTA AGG AAT GTT GCT CAC CTC GGA AGT TGG CAG	2638
Arg Phe Asp Pro Val Leu Arg Asn Val Ala His Leu Gly Ser Trp Gln	
865 870 875	
GTT ATA AGC CCG GTT GAA GTA TCA GGT TAT GTG GTT GTG GTT GAT GAG	2686
Val Ile Ser Pro Val Glu Val Ser Gly Tyr Val Val Val Val Asp Glu	
880 885 890 895	
TTA CTT GCT GTC CAG AAC AAA TCT TAT GAT AAA CCA ACC ATC CTT GTG	2734
Leu Leu Ala Val Gln Asn Lys Ser Tyr Asp Lys Pro Thr Ile Leu Val	
900 905 910	
GCA AAG AGT GTC AAG GGA GAG GAA GAA ATA CCA GAT GGA GTA GTT GGT	2782
Ala Lys Ser Val Lys Gly Glu Glu Glu Ile Pro Asp Gly Val Val Gly	
915 920 925	

101

GTA ATT ACA CCT GAT ATG CCA GAT GTT CTG TCT CAT GTG TCA GTC CGA	2830
Val Ile Thr Pro Asp Met Pro Asp Val Leu Ser His Val Ser Val Arg	
930 935 940	
GCA AGG AAT AGC AAG GTA CTG TTT GCG ACC TGT TTT GAC CAC ACC ACT	2878
Ala Arg Asn Ser Lys Val Leu Phe Ala Thr Cys Phe Asp His Thr Thr	
945 950 955	
CTA TCT GAA CTT GAA GGA TAT GAT CAG AAA CTG TTT TCC TTC AAG CCT	2926
Leu Ser Glu Leu Glu Gly Tyr Asp Gln Lys Leu Phe Ser Phe Lys Pro	
960 965 970 975	
ACT TCT GCA GAT ATA ACC TAT AGG GAG ATC ACA GAG AGT GAA CTT CAG	2974
Thr Ser Ala Asp Ile Thr Tyr Arg Glu Ile Thr Glu Ser Glu Leu Gln	
980 985 990	
CAA TCA AGT TCT CCA AAT GCA GAA GTT GGC CAT GCA GTA CCA TCT ATT	3022
Gln Ser Ser Ser Pro Asn Ala Glu Val Gly His Ala Val Pro Ser Ile	
995 1000 1005	
TCA TTG GCC AAG AAG AAA TTT CTT GGA AAA TAT GCA ATA TCA GCC GAA	3070
Ser Leu Ala Lys Lys Lys Phe Leu Gly Lys Tyr Ala Ile Ser Ala Glu	
1010 1015 1020	
GAA TTC TCT GAG GAA ATG GTT GGG GCC AAG TCT CGG AAT ATA GCA TAC	3118
Glu Phe Ser Glu Glu Met Val Gly Ala Lys Ser Arg Asn Ile Ala Tyr	
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CTC AAA GGA AAA GTA CCT TCA TGG GTC GGT GTC CCA ACG TCA GTT GCG	3166
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1040 1045 1050 1055	
ATA CCA TTT GGC ACT TTT GAG AAG GTT TTG TCA GAT GGG CTT AAT AAG	3214
Ile Pro Phe Gly Thr Phe Glu Lys Val Leu Ser Asp Gly Leu Asn Lys	
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1075 1080 1085	
GAT TTT AGT GCT CTA GGT GAA ATA AGA AAA GTC GTC CTT AAT CTT ACT	3310
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1090 1095 1100	
GCT CCT ATG CAA TTG GTT AAT GAG CTG AAG GAG AGG ATG CTA GGC TCT	3358
Ala Pro Met Gln Leu Val Asn Glu Leu Lys Glu Arg Met Leu Gly Ser	
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GGA ATG CCC TGG CCT GGT GAT GAA GGA GAC AAG CGT TGG GAG CAA GCA	3406
Gly Met Pro Trp Pro Gly Asp Glu Gly Asp Lys Arg Trp Glu Gln Ala	
1120 1125 1130 1135	
TGG ATG GCT ATT AAA AAG GTT TGG GCA TCA AAA TGG AAC GAA AGA GCA	3454
Trp Met Ala Ile Lys Lys Val Trp Ala Ser Lys Trp Asn Glu Arg Ala	
1140 1145 1150	
TAT TTT AGC ACA CGC AAG GTG AAA CTT GAT CAT GAG TAC CTT TCG ATG	3502
Tyr Phe Ser Thr Arg Lys Val Lys Leu Asp His Glu Tyr Leu Ser Met	
1155 1160 1165	

GCT GTT CTC GTG CAA GAA GTT GTG AAT GCA GAT TAT GCT TTT GTC ATT Ala Val Leu Val Gln Glu Val Val Asn Ala Asp Tyr Ala Phe Val Ile 1170 1175 1180	3550
CAT ACC ACA AAC CCA TCG TCT GGA GAT TCT TCT GAG ATA TAT GCT GAA His Thr Thr Asn Pro Ser Ser Gly Asp Ser Ser Glu Ile Tyr Ala Glu 1185 1190 1195	3598
GTG GTG AAA GGG CTT GGC GAG ACC CTC GTG GGA GCC TAT CCT GGT CGT Val Val Lys Gly Leu Gly Glu Thr Leu Val Gly Ala Tyr Pro Gly Arg 1200 1205 1210 1215	3646
GCT ATG AGC TTT GTT TGC AAA AAA GAT GAC CTT GAC TCT CCC AAG TTA Ala Met Ser Phe Val Cys Lys Lys Asp Asp Leu Asp Ser Pro Lys Leu 1220 1225 1230	3694
CTT GGT TAC CCA AGC AAG CCA ATT GGT CTC TTC ATA AGG CAA TCA ATC Leu Gly Tyr Pro Ser Lys Pro Ile Gly Leu Phe Ile Arg Gln Ser Ile 1235 1240 1245	3742
ATC TTC CGT TCC GAC TCC AAC GGT GAG GAC CTG GAA GGT TAT GCT GGA Ile Phe Arg Ser Asp Ser Asn Gly Glu Asp Leu Glu Gly Tyr Ala Gly 1250 1255 1260	3790
GCA GGA TTA TAT GAT AGT GTA CCG ATG GAT GAG GAG GAT GAG GTT GTA Ala Gly Leu Tyr Asp Ser Val Pro Met Asp Glu Glu Asp Glu Val Val 1265 1270 1275	3838
CTT GAT TAT ACA ACT GAC CCT CTT ATA GTA GAC CGT GGA TTC CGA AGC Leu Asp Tyr Thr Thr Asp Pro Leu Ile Val Asp Arg Gly Phe Arg Ser 1280 1285 1290 1295	3886
TCA ATC CTC TCA AGC ATA GCA CGG GCT GGC CAT GCC ATC GAG GAG CTA Ser Ile Leu Ser Ser Ile Ala Arg Ala Gly His Ala Ile Glu Glu Leu 1300 1305 1310	3934
TAT GGT TCT CCT CAG GAC GTC GAG GGA GTA GTG AAG GAT GGA AAA ATC Tyr Gly Ser Pro Gln Asp Val Glu Gly Val Val Lys Asp Gly Lys Ile 1315 1320 1325	3982
TAT GTA GTC CAG ACA AGA CCA CAG ATG TAGTATGTAT GCATCTATTA Tyr Val Val Gln Thr Arg Pro Gln Met 1330 1335	4029
GACAGCTCAA TAAGCACTGT TGTACGCTTG TATGGTTGGG ACATATGGGC GTTATGGCAT	4089
GTATAGTTGT ATGCCTAGAT GTACAACACG TGTACTCGTA TATATATATA TAAATGCTGA	4149
AACAAGCATT GGTCTGTAC TGTAGTTTCT ACATTTTCATT GTCACCAATA ATTAAGTGTA	4209
CTCCTATGGC TGGGAGTCTA TGAAAATGGA CGTGTGACT TATTGGGTAA TAAATAATTT	4269
ATATATAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	4329

(2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1336 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

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Pro Asp Gly Thr Thr Val Tyr Lys Asn Arg Ala Leu Arg Thr Pro Phe
 1      5      10      15
Val Lys Ser Gly Asp Asn Ser Thr Leu Arg Ile Glu Ile Asp Asp Pro
      20      25      30
Gly Val His Ala Ile Glu Phe Leu Ile Phe Asp Glu Thr Gln Asn Lys
      35      40      45
Trp Phe Lys Asn Asn Gly Gln Asn Phe Gln Val Gln Phe Gln Ser Ser
      50      55      60
Arg His Gln Gly Thr Gly Ala Ser Gly Ala Ser Ser Ser Ala Thr Ser
      65      70      75      80
Thr Leu Val Pro Glu Asp Leu Val Gln Ile Gln Ala Tyr Leu Arg Trp
      85      90      95
Glu Arg Arg Gly Lys Gln Ser Tyr Thr Pro Glu Gln Glu Lys Glu Glu
      100      105      110
Tyr Glu Ala Ala Arg Ala Glu Leu Ile Glu Glu Val Asn Arg Gly Val
      115      120      125
Ser Leu Glu Lys Leu Arg Ala Lys Leu Thr Lys Ala Pro Glu Ala Pro
      130      135      140
Glu Ser Asp Glu Ser Lys Ser Ser Ala Ser Arg Val Pro Ile Gly Lys
      145      150      155      160
Leu Pro Glu Asp Leu Val Gln Val Gln Ala Tyr Ile Arg Trp Glu Gln
      165      170      175
Ala Gly Lys Pro Asn Tyr Pro Pro Glu Lys Gln Leu Val Glu Phe Glu
      180      185      190
Glu Ala Arg Lys Glu Leu Gln Ala Glu Val Asp Lys Gly Ile Ser Ile
      195      200      205
Asp Gln Leu Arg Gln Lys Ile Leu Lys Gly Asn Ile Glu Ser Lys Val
      210      215      220
Ser Lys Gln Leu Lys Asn Lys Lys Tyr Phe Ser Val Glu Arg Ile Gln
      225      230      235      240
Arg Lys Lys Arg Asp Ile Thr Gln Leu Leu Ser Lys His Lys His Thr
      245      250      255
Val Met Glu Asp Lys Val Glu Val Val Pro Lys Gln Pro Thr Val Leu
      260      265      270
Asp Leu Phe Thr Lys Ser Leu His Glu Lys Asp Gly Cys Glu Val Leu
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Ser Arg Lys Leu Phe Lys Phe Gly Asp Lys Glu Ile Leu Ala Ile Ser
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Thr Lys Val Gln Asn Lys Thr Glu Val His Leu Ala Thr Asn His Thr
 305 310 315 320
 Asp Pro Leu Ile Leu His Trp Ser Leu Ala Lys Asn Ala Gly Glu Trp
 325 330 335
 Lys Ala Pro Ser Pro Asn Ile Leu Pro Ser Gly Ser Thr Leu Leu Asp
 340 345 350
 Lys Ala Cys Glu Thr Glu Phe Thr Lys Ser Glu Leu Asp Gly Leu His
 355 360 365
 Tyr Gln Val Val Glu Ile Glu Leu Asp Asp Gly Gly Tyr Lys Gly Met
 370 375 380
 Pro Phe Val Leu Arg Ser Gly Glu Thr Trp Ile Lys Asn Asn Gly Ser
 385 390 395 400
 Asp Phe Phe Leu Asp Phe Ser Thr His Asp Val Arg Asn Ile Lys Ala
 405 410 415
 Ile Leu Lys Asp Asn Gly Asp Ala Gly Lys Gly Thr Ser Lys Ala Leu
 420 425 430
 Leu Glu Arg Ile Ala Asp Leu Glu Glu Asp Ala Gln Arg Ser Leu Met
 435 440 445
 His Arg Phe Asn Ile Ala Ala Asp Leu Ala Asp Gln Ala Arg Asp Ala
 450 455 460
 Gly Leu Leu Gly Ile Val Gly Leu Phe Val Trp Ile Arg Phe Met Ala
 465 470 475 480
 Thr Arg Gln Leu Thr Trp Asn Lys Asn Tyr Asn Val Lys Pro Arg Glu
 485 490 495
 Ile Ser Lys Ala Gln Asp Arg Phe Thr Asp Asp Leu Glu Asn Met Tyr
 500 505 510
 Lys Thr Tyr Pro Gln Tyr Arg Glu Ile Leu Arg Met Ile Met Ala Ala
 515 520 525
 Val Gly Arg Gly Gly Glu Gly Asp Val Gly Gln Arg Ile Arg Asp Glu
 530 535 540
 Ile Leu Val Ile Gln Arg Asn Asn Asp Cys Lys Gly Gly Met Met Glu
 545 550 555 560
 Glu Trp His Gln Lys Leu His Asn Asn Thr Ser Pro Asp Asp Val Val
 565 570 575
 Ile Cys Gln Ala Leu Ile Asp Tyr Ile Lys Ser Asp Phe Asp Ile Ser
 580 585 590
 Val Tyr Trp Asp Thr Leu Asn Lys Asn Gly Ile Thr Lys Glu Arg Leu
 595 600 605
 Leu Ser Tyr Asp Arg Ala Ile His Ser Glu Pro Asn Phe Arg Ser Glu
 610 615 620
 Gln Lys Ala Gly Leu Leu Arg Asp Leu Gly Asn Tyr Met Arg Ser Leu
 625 630 635 640

Lys Ala Val His Ser Gly Ala Asp Leu Glu Ser Ala Ile Ala Ser Cys
 645 650 655
 Met Gly Tyr Lys Ser Glu Gly Glu Gly Phe Met Val Gly Val Gln Ile
 660 665 670
 Asn Pro Val Lys Gly Leu Pro Ser Gly Phe Pro Glu Leu Leu Glu Phe
 675 680 685
 Val Leu Glu His Val Glu Asp Lys Ser Ala Glu Pro Leu Pro Glu Gly
 690 695 700
 Leu Leu Glu Ala Arg Val Glu Leu Arg Pro Leu Leu Leu Asp Ser Arg
 705 710 715 720
 Glu Arg Met Lys Asp Leu Ile Phe Leu Asp Ile Ala Leu Asp Ser Thr
 725 730 735
 Phe Arg Thr Ala Ile Glu Arg Ser Tyr Glu Glu Leu Asn Asp Ala Ala
 740 745 750
 Pro Glu Lys Ile Met Tyr Phe Ile Ser Leu Val Leu Glu Asn Leu Ala
 755 760 765
 Leu Ser Ile Asp Asp Asn Glu Asp Ile Leu Tyr Cys Leu Lys Gly Trp
 770 775 780
 Asn Gln Ala Leu Glu Met Ala Lys Gln Lys Asp Asp Gln Trp Ala Leu
 785 790 795 800
 Tyr Ala Lys Ala Phe Leu Asp Arg Asn Arg Leu Ala Leu Ala Ser Lys
 805 810 815
 Gly Glu Gln Tyr His Asn Met Met Gln Pro Ser Ala Glu Tyr Leu Gly
 820 825 830
 Ser Leu Leu Ser Ile Asp Gln Trp Ala Val Asn Ile Phe Thr Glu Glu
 835 840 845
 Ile Ile Arg Gly Gly Ser Ala Ala Thr Leu Ser Ala Leu Leu Asn Arg
 850 855 860
 Phe Asp Pro Val Leu Arg Asn Val Ala His Leu Gly Ser Trp Gln Val
 865 870 875 880
 Ile Ser Pro Val Glu Val Ser Gly Tyr Val Val Val Val Asp Glu Leu
 885 890 895
 Leu Ala Val Gln Asn Lys Ser Tyr Asp Lys Pro Thr Ile Leu Val Ala
 900 905 910
 Lys Ser Val Lys Gly Glu Glu Glu Ile Pro Asp Gly Val Val Gly Val
 915 920 925
 Ile Thr Pro Asp Met Pro Asp Val Leu Ser His Val Ser Val Arg Ala
 930 935 940
 Arg Asn Ser Lys Val Leu Phe Ala Thr Cys Phe Asp His Thr Thr Leu
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106

Ser Glu Leu Glu Gly Tyr Asp Gln Lys Leu Phe Ser Phe Lys Pro Thr
 965 970 975

Ser Ala Asp Ile Thr Tyr Arg Glu Ile Thr Glu Ser Glu Leu Gln Gln
 980 985 990

Ser Ser Ser Pro Asn Ala Glu Val Gly His Ala Val Pro Ser Ile Ser
 995 1000 1005

Leu Ala Lys Lys Lys Phe Leu Gly Lys Tyr Ala Ile Ser Ala Glu Glu
 1010 1015 1020

Phe Ser Glu Glu Met Val Gly Ala Lys Ser Arg Asn Ile Ala Tyr Leu
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Lys Gly Lys Val Pro Ser Trp Val Gly Val Pro Thr Ser Val Ala Ile
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Pro Phe Gly Thr Phe Glu Lys Val Leu Ser Asp Gly Leu Asn Lys Glu
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Phe Ser Ala Leu Gly Glu Ile Arg Lys Val Val Leu Asn Leu Thr Ala
 1090 1095 1100

Pro Met Gln Leu Val Asn Glu Leu Lys Glu Arg Met Leu Gly Ser Gly
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Met Ala Ile Lys Lys Val Trp Ala Ser Lys Trp Asn Glu Arg Ala Tyr
 1140 1145 1150

Phe Ser Thr Arg Lys Val Lys Leu Asp His Glu Tyr Leu Ser Met Ala
 1155 1160 1165

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 1170 1175 1180

Thr Thr Asn Pro Ser Ser Gly Asp Ser Ser Glu Ile Tyr Ala Glu Val
 1185 1190 1195 1200

Val Lys Gly Leu Gly Glu Thr Leu Val Gly Ala Tyr Pro Gly Arg Ala
 1205 1210 1215

Met Ser Phe Val Cys Lys Lys Asp Asp Leu Asp Ser Pro Lys Leu Leu
 1220 1225 1230

Gly Tyr Pro Ser Lys Pro Ile Gly Leu Phe Ile Arg Gln Ser Ile Ile
 1235 1240 1245

Phe Arg Ser Asp Ser Asn Gly Glu Asp Leu Glu Gly Tyr Ala Gly Ala
 1250 1255 1260

Gly Leu Tyr Asp Ser Val Pro Met Asp Glu Glu Asp Glu Val Val Leu
 1265 1270 1275 1280

Asp Tyr Thr Thr Asp Pro Leu Ile Val Asp Arg Gly Phe Arg Ser Ser
 1285 1290 1295

Ile Leu Ser Ser Ile Ala Arg Ala Gly His Ala Ile Glu Glu Leu Tyr
1300 1305 1310

Gly Ser Pro Gln Asp Val Glu Gly Val Val Lys Asp Gly Lys Ile Tyr
1315 1320 1325

Val Val Gln Thr Arg Pro Gln Met
1330 1335

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

- (iii) HYPOTHETICAL: YES

- (iv) ANTI-SENSE: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GCAAAGTTTT CAAGGACAAG ACTGATGAAG

30

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

- (iii) HYPOTHETICAL: YES

- (iv) ANTI-SENSE: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

CCAGATGGCA CGACAGTGTA CAAGAACA

28

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: modified_base
(B) LOCATION:15
(D) OTHER INFORMATION:/mod_base= i

(ix) FEATURE:

(A) NAME/KEY: modified_base
(B) LOCATION:18
(D) OTHER INFORMATION:/mod_base= i

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

AATGACTGCA AAGGGGGGAT GATGGA

Claims

1. A nucleic acid molecule encoding a protein from maize which is present in plant cells in starch granule-bound form as well as in soluble form, selected from the group consisting of:
 - (a) nucleic acid molecules encoding a protein comprising the amino acid sequence indicated as in Seq ID No. 6 or in Seq ID No. 8;
 - (b) nucleic acid molecules comprising the coding region of the nucleotide sequences indicated under Seq ID No. 5 or under Seq ID No. 7; and
 - (c) nucleic acid molecules hybridizing to the complementary strand of a nucleic acid molecules indicated under (a) or (b); and
 - (d) nucleic acid molecules the sequence of which differs from the sequence of a nucleic acid molecule of any one of (a) to (c) due to the degeneracy of the genetic code;as well as the respective complementary strand of such a nucleic acid molecule.
2. A vector containing a nucleic acid molecule of claim 1.
3. The vector of claim 2, wherein the nucleic acid molecule is linked to regulatory elements ensuring transcription in eukaryotic and prokaryotic cells.
4. A host cell, which is genetically modified with a nucleic acid molecule of claim 1 or with a vector of claim 2 or 3.
5. The host cell of claim 4, being a transgenic plant cell.
6. A plant containing the plant cell of claim 5.

7. A process for the production of a modified starch comprising the step of extracting from plants of claim 6 and/or from starch storing parts of such plants the starch.
8. Starch obtainable from a plant cell of claim 5, from a plant of claim 6 or by the process of claim 7.
9. A method for the production of a protein from maize in which a host cell of claim 4 is cultivated under conditions allowing for the expression of the protein and in which the protein is isolated from the cells and/or the culture medium.
10. A protein encoded by a nucleic acid molecule of claim 1 or obtainable by the method of claim 9.
11. An antibody specifically recognizing the protein of claim 10.
12. A nucleic acid molecule with a length of at least 15 nucleotides which specifically hybridizes to a nucleic acid molecule of claim 1.
13. A DNA molecule encoding an antisense-RNA complementary to the transcripts of a DNA molecule according to claim 1.
14. A DNA molecule encoding an RNA with ribozyme activity which specifically cleaves transcripts of a DNA molecule of claim 1.
15. A DNA molecule encoding an RNA which upon expression in a plant cell leads to a reduction of the expression of a

nucleic acid molecule of claim 1, due to a cosuppression effect.

16. A vector containing a DNA molecule of any one of claims 13 to 15.
17. The vector of claim 16, wherein the DNA molecule is combined with regulatory DNA elements ensuring transcription in plant cells.
18. A host cell containing a DNA molecule of any one of claims 13 to 15 or a vector of claim 16 or 17.
19. A transgenic plant cell containing a DNA molecule of any one of claims 13 to 15 in combination with regulatory DNA elements ensuring transcription in plant cells.
20. The transgenic plant cell of claim 19, in which the activity of at least one further enzyme involved in the starch biosynthesis or modification is reduced when compared to non-transformed plants.
21. The transgenic plant cell of claim 20 in which the activity of a branching enzyme is reduced.
22. The transgenic plant cell of claim 21 in which the activity of a starch granule-bound starch synthase of the isotype I (GBSS I) is reduced.
23. A transgenic plant containing a plant cell of any one of claims 19 to 22.
24. An RNA molecule obtainable by transcription of a DNA molecule of any one of claims 13 to 15.

25. A method for the production of transgenic plant cells synthesizing a modified starch characterized in that the amount of proteins of claim 11, which are synthesized in the cells in endogenous form, is reduced in the cells.
26. The method of claim 25 characterized in that the reduction of the amount of proteins of claim 11 in the cells is caused by an antisense effect.
27. The method of claim 25 characterized in that the reduction of the amount of proteins of claim 11 in the cells is caused by a ribozyme effect.
28. The method of claim 25 characterized in that the reduction of the amount of proteins of claim 11 in the cells is caused by a cosuppression effect.
29. The method of any one of claims 25 to 28, wherein the enzyme activity of at least one further enzyme involved in the starch biosynthesis and/or modification is reduced.
30. The method of claim 29 wherein the enzyme is a branching enzyme.
31. The method of claim 29 wherein the enzyme is a starch granule-bound starch synthase of the isotype I (GBSSI).
32. A plant cell obtainable by a method of any one of claims 25 to 31.
33. A transgenic plant containing plant cells of claim 32.
34. A process for the production of a modified starch comprising the step of extracting from the plant of claim

- 23 or 33 and/or from a starch storing part of such a plant the starch.
35. Starch obtainable from plant cells of any one of claim 19 to 22 or of claim 32, of a plant of claim 23 or 33 or by the process of claim 35.
36. The starch of claim 35 characterized in that it is derived from maize.
37. Propagation material of plants of claim 6 containing plant cells of claim 5.
38. The propagation material of plants of claim 23 or 33, containing plant cells of any one of claims 19 to 22 or of claim 32.
39. The transgenic plant of claim 23 or 33 which is a maize plant.
40. Seeds of a maize plant of claim 39.

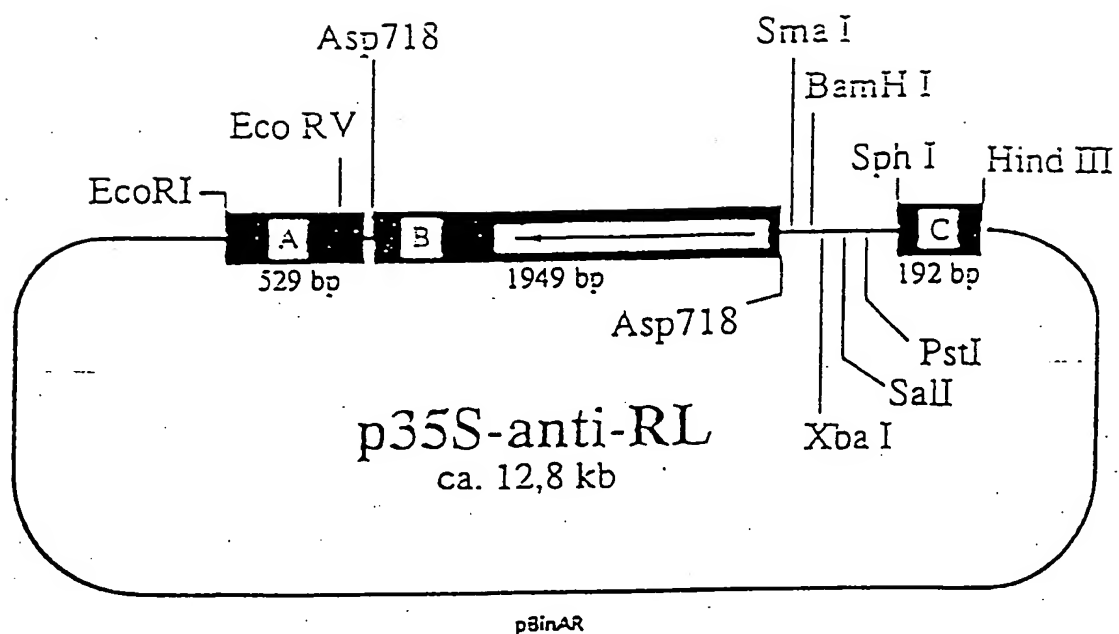


Fig. 1

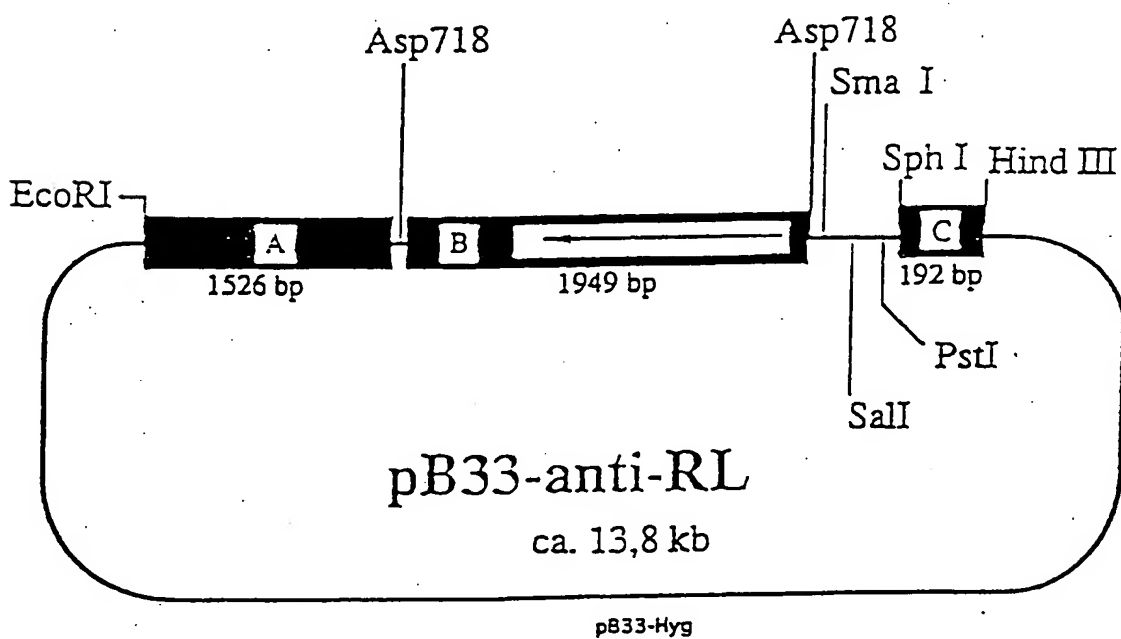


Fig. 2

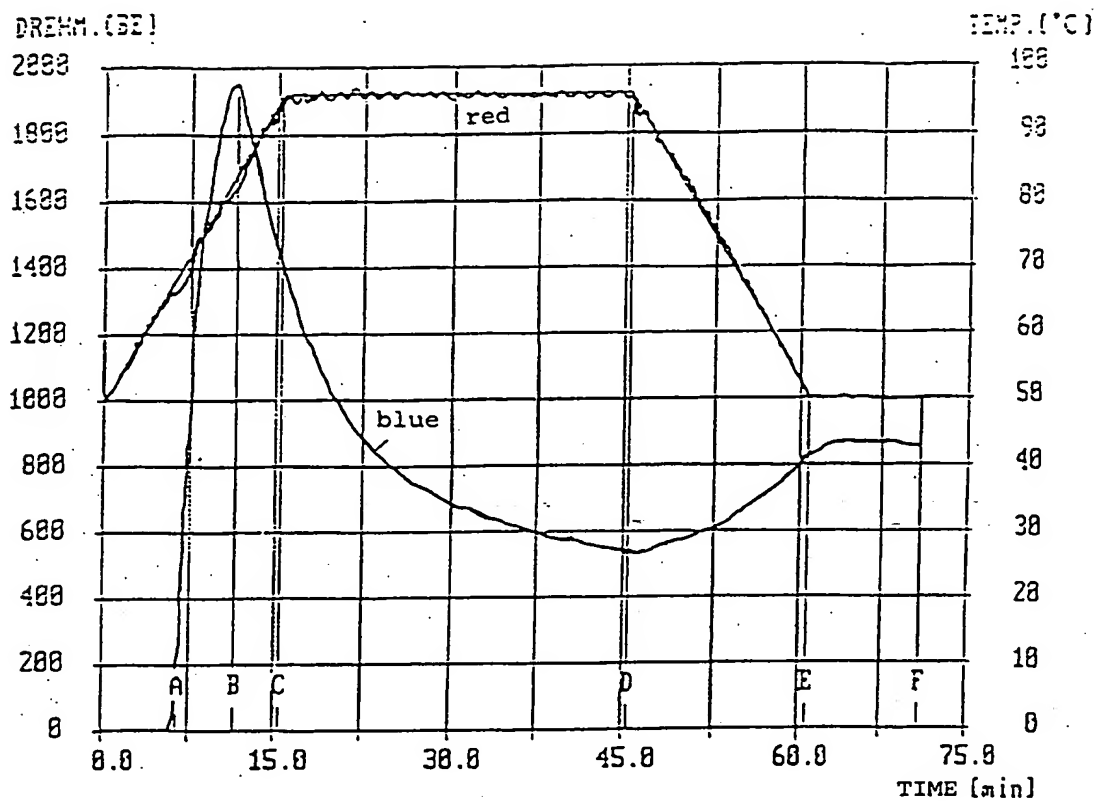


Figure 3

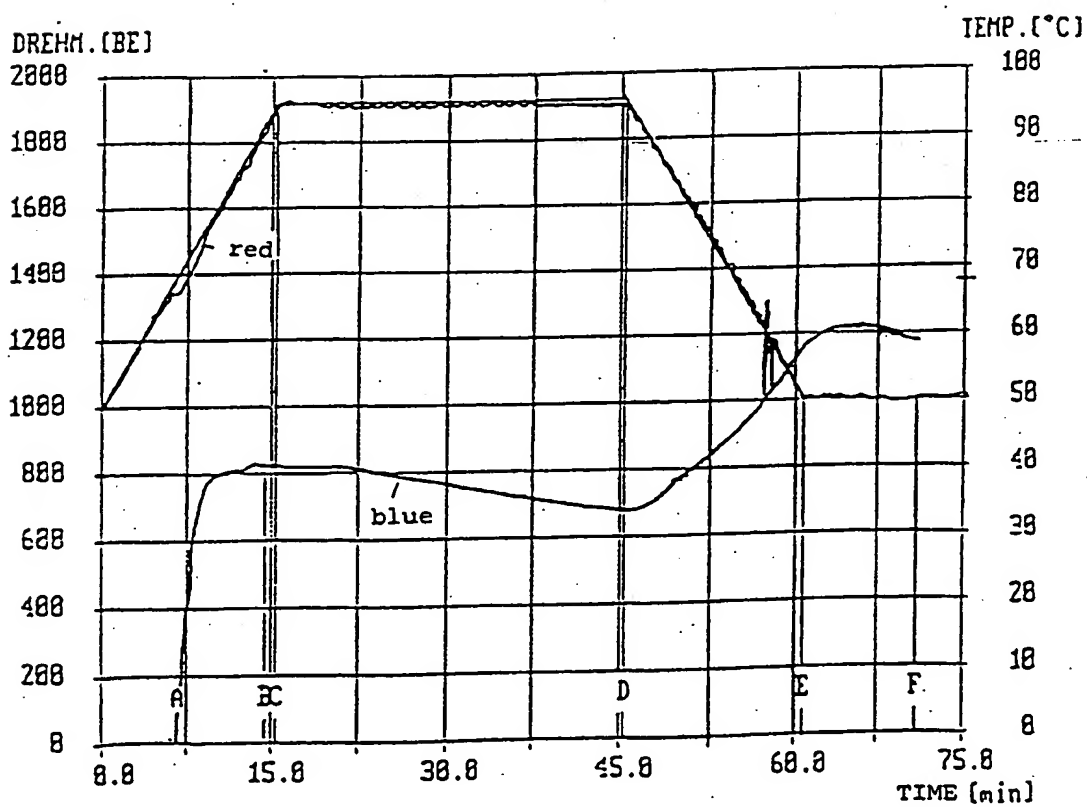


Figure 4

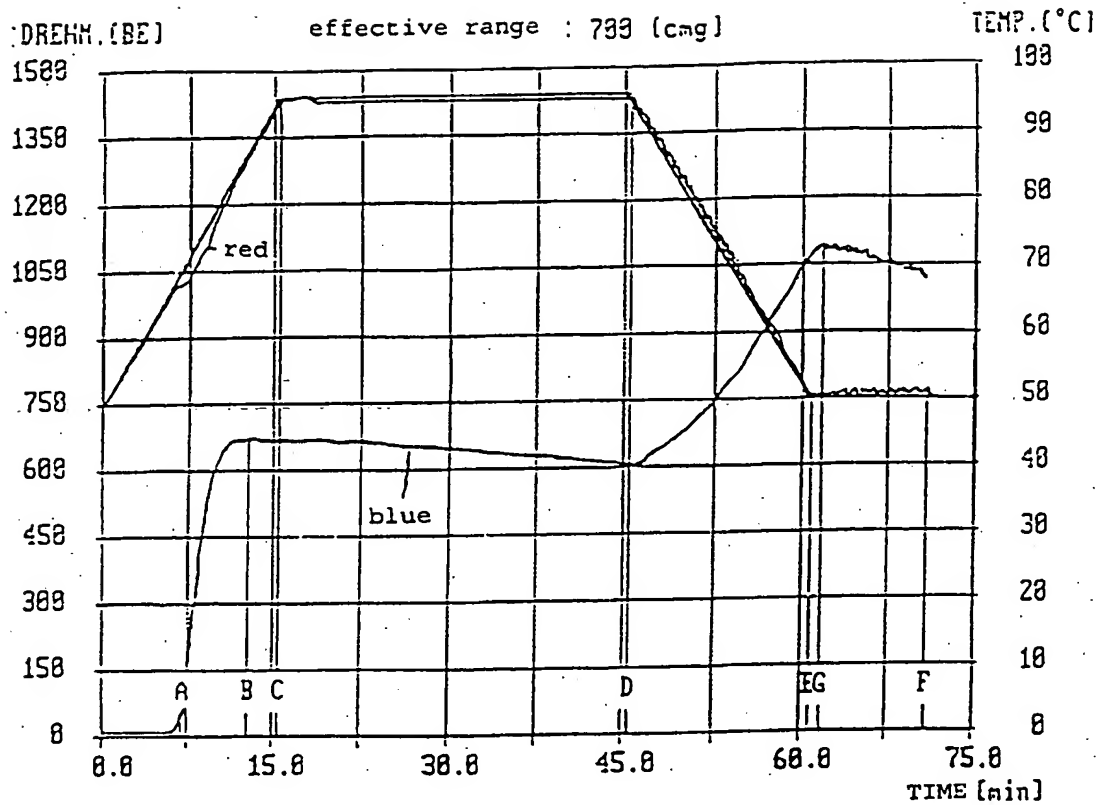


Figure 5

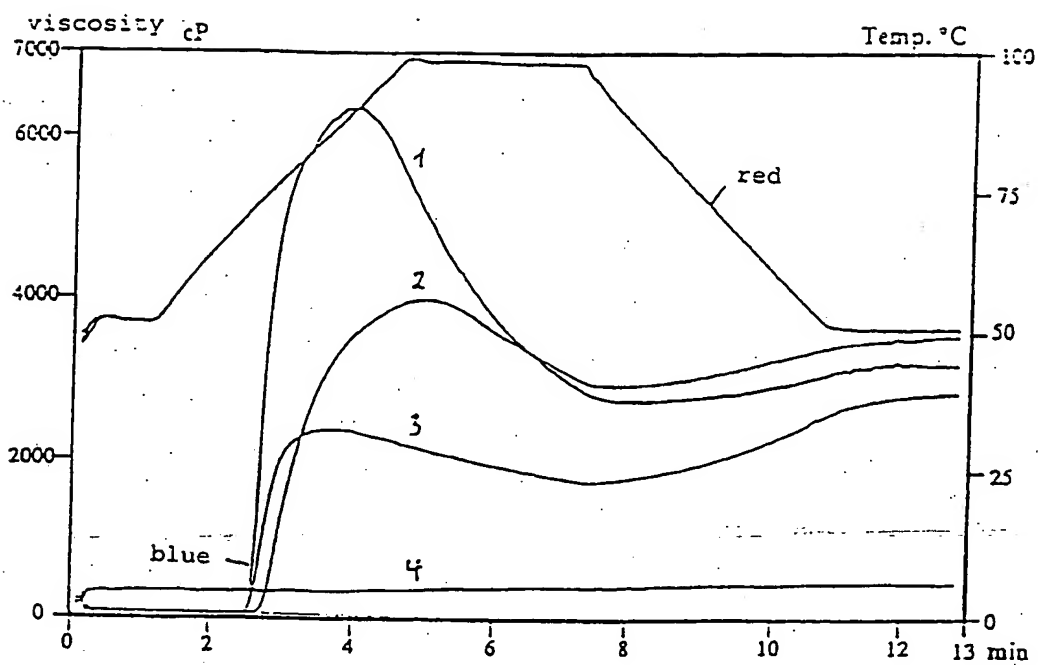


Figure 6

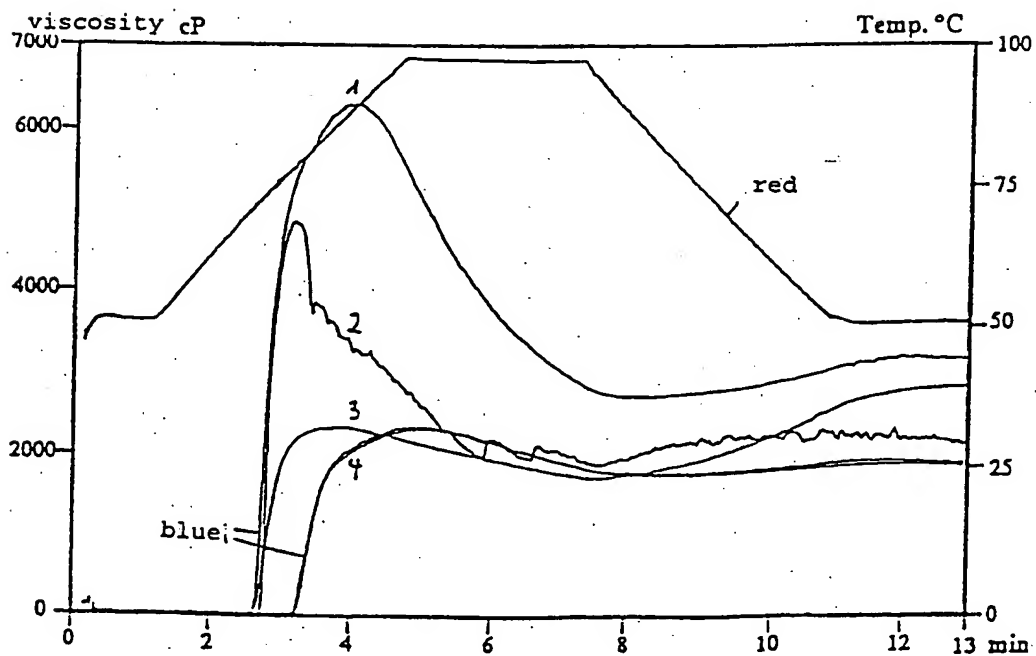


Figure 7

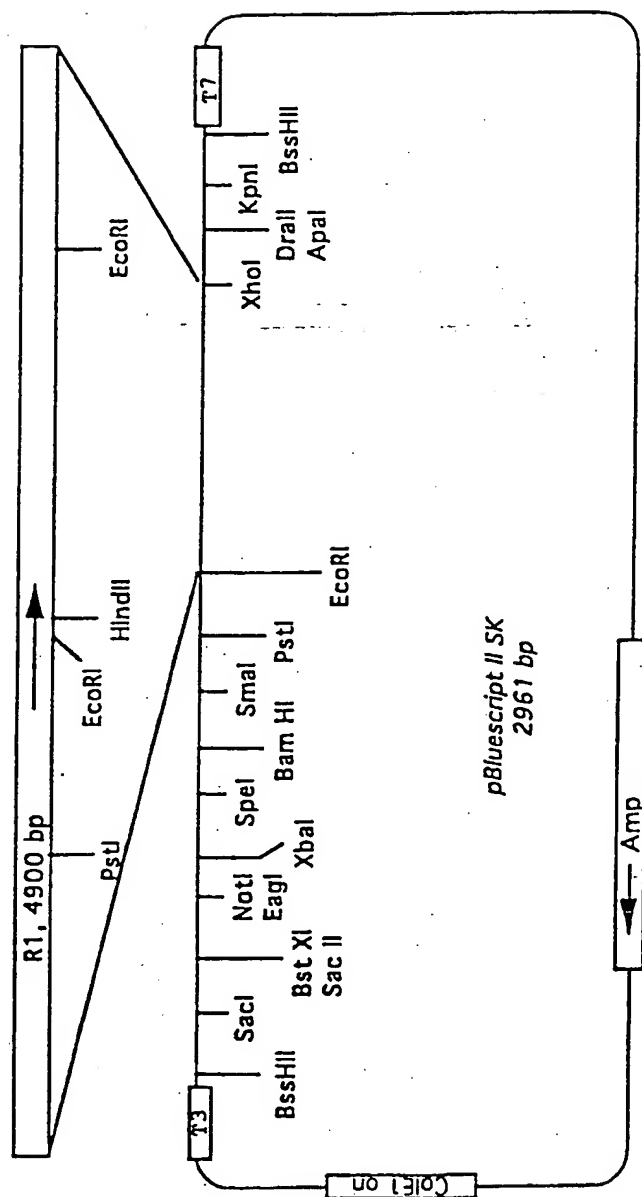


Figure 8

INTERNATIONAL SEARCH REPORT

International Application No

PC1/EP 97/07123

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/29 C12N15/54 C12N15/82 C12N15/10 C12N5/10
C08B30/00 C07K14/415 C07K16/16 A01H5/00 A23L1/0522

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N C07K C08B A01H A23L

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X A	WO 94 09144 A (ZENECA LTD) 28 April 1994 see the whole document	8, 35, 36 1-7, 9-34, 37-40
X A	WO 95 07355 A (INST GENBIOLOGISCHE FORSCHUNG ; KOSSMANN JENS (DE); VIRGIN IVAR (DE) 16 March 1995 cited in the application see the whole document	8, 35, 36 20, 21, 23, 34, 38-40

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☒ Further documents are listed in the continuation of box C.

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14 April 1998

Date of mailing of the international search report

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INTERNATIONAL SEARCH REPORT

International Application No

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C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 96 15248 A (INST GENBIOLOGISCHE FORSCHUNG ;KOSSMANN JENS (DE); SPRINGER FRANZI) 23 May 1996	8, 35, 36
A	see the whole document	20, 22, 23, 34, 38-40
P, X	WO 97 11188 A (KOSSMANN JENS ;LORBERTH RUTH (DE); PLANTTEC BIOTECHNOLOGIE GMBH (D) 27 March 1997 see the whole document	8, 35, 36

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/EP 97/07123

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9409144 A	28-04-94	AU 2696492 A EP 0664835 A	09-05-94 02-08-95
WO 9507355 A	16-03-95	DE 4330960 A AU 7657394 A EP 0719338 A JP 9502098 T CA 2171313 A HU 74667 A	16-03-95 27-03-95 03-07-96 04-03-97 16-03-95 28-01-97
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